

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (II) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention.
CC Note: The present sequence did not form part of the printed
CC specification, but is based on sequence information supplied to Derwent
CC by the European Patent Office.

XX SQ Sequence 17 BP; 8 A; 2 C; 6 G; 1 T; 0 other;
XX Query Match 61.0%; Score 12.8; DB 24; Length 17;
XX Best Local Similarity 87.5%; Pred. No. 3.2e+04;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCTCACCCCTTGCTCT 19
DB 16 TTCTCACTCTTGCTCT 1

RESULT 15
AAA79747/C
ID AAA79747 standard; DNA; 20 BP.

XX AC AAA79747;

XX DT 20-NOV-2000 (first entry)

XX DE Hepatitis B virus related oligonucleotide probe #10.

XX KW Hepatitis B virus; HBV; Hepatitis A virus; HAV; probe; detection;
XX KW mutation; high-density gene chip; ss.

XX OS Hepatitis B virus.

XX PN CN1252452-A.

XX PD 10-MAY-2000.

XX PF 24-SEP-1999; 99CN-0114460.

XX PR 24-SEP-1999; 99CN-0114460.

XX PA (UYDO-) UNIV DONGNAN.

XX PI Sun X, Lu Z, Wang Y;

XX DR WPI; 2000-443233/39.

XX High-density gene chip making process -

XX Example 1; Fig 15; 19pp; Chinese.

CC The present invention describes a method which comprises making a high-
CC density gene chip, specifically for making high-density micro-array of
CC oligonucleotide probes. An oligonucleotide probe selecting process to
CC seek preferentially length variable and coverage variable probes is
CC provided to ensure identical cross melting temperature of probes to the
CC maximum limit, and this can make the cross control of gene chip
CC relatively simple and raise the reliability of the gene chip detecting
CC results. The process proposes a specific probe selection method for
CC detecting target sequence directly, detecting mutation in both specific
CC and non-specific sites and a probe overall arrangement scheme. AAA79738
CC to AAA80201 represent oligonucleotide probe sequences which are used in
CC examples from the present invention.

XX

SQ Sequence 20 BP; 8 A; 1 C; 9 G; 2 T; 0 other;

Query Match 61.0%; Score 12.8; DB 21; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCTCACCCCTTGCTCT 19
DB 19 TCCTAACCCCTTGCTCT 4

Search completed: February 20, 2004, 00:55:57
Job time : 173 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 00:32:29, Search time 1490 Seconds
(without alignments)
342.546 Million cell updates/sec

Title: US-10-085-108-21_COPY_175_195

Perfect score: 21

Sequence: 1 TCATCCTCACCCCTGTCTCTCA 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 8380

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_esthm:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vit:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	57.1	21	28	AZ321746 IM0042N20
2	11	52.4	19	28	AZ775540 2M0008H15
3	10.4	49.5	20	28	AZ829601 2M0107D03
4	10.4	49.5	21	28	AZ580960 IM0369P04

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	TITLE	JOURNAL COMMENT
AZ321746/c	21 bp	DNA	linear	GSS	29-SEP-2000			
IM0042N20F	Mouse 10kb	plasmid	U9C1M	library	Mus musculus genomic			
clone U9C1M0042N20 F	genomic	survey	sequence.					
AZ321746								
AZ321746.1	GT:10374795							
GSS.								
Mus musculus	(house mouse)							
Mus musculus								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
1 (bases 1 to 21)								
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.								
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts								
Unpublished								
Contact: Robert B. Weiss								
University of Utah Genome Center								
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA								
Tel: 801 585 5606								
Fax: 801 585 7177								

ALIGNMENTS

5	10	47.6	21	28	AZ313243	AZ313243	IM0029H16
6 <td>10<td>47.6<td>21<td>28<td>AZ849030<td>AZ849030<td>IM0150I17</td></td></td></td></td></td></td>	10 <td>47.6<td>21<td>28<td>AZ849030<td>AZ849030<td>IM0150I17</td></td></td></td></td></td>	47.6 <td>21<td>28<td>AZ849030<td>AZ849030<td>IM0150I17</td></td></td></td></td>	21 <td>28<td>AZ849030<td>AZ849030<td>IM0150I17</td></td></td></td>	28 <td>AZ849030<td>AZ849030<td>IM0150I17</td></td></td>	AZ849030 <td>AZ849030<td>IM0150I17</td></td>	AZ849030 <td>IM0150I17</td>	IM0150I17
7 <td>9.8<td>45.7<td>13<td>12<td>BG926067<td>BG926067<td>HNC23-1-E</td></td></td></td></td></td></td>	9.8 <td>45.7<td>13<td>12<td>BG926067<td>BG926067<td>HNC23-1-E</td></td></td></td></td></td>	45.7 <td>13<td>12<td>BG926067<td>BG926067<td>HNC23-1-E</td></td></td></td></td>	13 <td>12<td>BG926067<td>BG926067<td>HNC23-1-E</td></td></td></td>	12 <td>BG926067<td>BG926067<td>HNC23-1-E</td></td></td>	BG926067 <td>BG926067<td>HNC23-1-E</td></td>	BG926067 <td>HNC23-1-E</td>	HNC23-1-E
8 <td>9.8<td>45.7<td>21<td>28<td>AZ654730<td>AZ654730<td>IM0529P05</td></td></td></td></td></td></td>	9.8 <td>45.7<td>21<td>28<td>AZ654730<td>AZ654730<td>IM0529P05</td></td></td></td></td></td>	45.7 <td>21<td>28<td>AZ654730<td>AZ654730<td>IM0529P05</td></td></td></td></td>	21 <td>28<td>AZ654730<td>AZ654730<td>IM0529P05</td></td></td></td>	28 <td>AZ654730<td>AZ654730<td>IM0529P05</td></td></td>	AZ654730 <td>AZ654730<td>IM0529P05</td></td>	AZ654730 <td>IM0529P05</td>	IM0529P05
9 <td>9.8<td>45.7<td>21<td>28<td>AZ657586<td>AZ657586<td>IM053D24</td></td></td></td></td></td></td>	9.8 <td>45.7<td>21<td>28<td>AZ657586<td>AZ657586<td>IM053D24</td></td></td></td></td></td>	45.7 <td>21<td>28<td>AZ657586<td>AZ657586<td>IM053D24</td></td></td></td></td>	21 <td>28<td>AZ657586<td>AZ657586<td>IM053D24</td></td></td></td>	28 <td>AZ657586<td>AZ657586<td>IM053D24</td></td></td>	AZ657586 <td>AZ657586<td>IM053D24</td></td>	AZ657586 <td>IM053D24</td>	IM053D24
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12 <td>9.6<td>45.7<td>19<td>28<td>AZ432757</td><td>AZ432757</td><td>wc74e09.x</td></td></td></td></td>	9.6 <td>45.7<td>19<td>28<td>AZ432757</td><td>AZ432757</td><td>wc74e09.x</td></td></td></td>	45.7 <td>19<td>28<td>AZ432757</td><td>AZ432757</td><td>wc74e09.x</td></td></td>	19 <td>28<td>AZ432757</td><td>AZ432757</td><td>wc74e09.x</td></td>	28 <td>AZ432757</td> <td>AZ432757</td> <td>wc74e09.x</td>	AZ432757	AZ432757	wc74e09.x
13 <td>9.6<td>45.7<td>19<td>28<td>AZ654214</td><td>AZ654214</td><td>IM0218L14</td></td></td></td></td>	9.6 <td>45.7<td>19<td>28<td>AZ654214</td><td>AZ654214</td><td>IM0218L14</td></td></td></td>	45.7 <td>19<td>28<td>AZ654214</td><td>AZ654214</td><td>IM0218L14</td></td></td>	19 <td>28<td>AZ654214</td><td>AZ654214</td><td>IM0218L14</td></td>	28 <td>AZ654214</td> <td>AZ654214</td> <td>IM0218L14</td>	AZ654214	AZ654214	IM0218L14
14 <td>9.6<td>45.7<td>19<td>28<td>AZ941399</td><td>AZ941399</td><td>IM0528H13</td></td></td></td></td>	9.6 <td>45.7<td>19<td>28<td>AZ941399</td><td>AZ941399</td><td>IM0528H13</td></td></td></td>	45.7 <td>19<td>28<td>AZ941399</td><td>AZ941399</td><td>IM0528H13</td></td></td>	19 <td>28<td>AZ941399</td><td>AZ941399</td><td>IM0528H13</td></td>	28 <td>AZ941399</td> <td>AZ941399</td> <td>IM0528H13</td>	AZ941399	AZ941399	IM0528H13
15 <td>9.6<td>45.7<td>20<td>28<td>AZ832404</td><td>AZ832404</td><td>2M0201P07</td></td></td></td></td>	9.6 <td>45.7<td>20<td>28<td>AZ832404</td><td>AZ832404</td><td>2M0201P07</td></td></td></td>	45.7 <td>20<td>28<td>AZ832404</td><td>AZ832404</td><td>2M0201P07</td></td></td>	20 <td>28<td>AZ832404</td><td>AZ832404</td><td>2M0201P07</td></td>	28 <td>AZ832404</td> <td>AZ832404</td> <td>2M0201P07</td>	AZ832404	AZ832404	2M0201P07
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17 <td>9.6<td>45.7<td>21<td>28<td>AZ978966</td><td>AZ978966</td><td>2M0092B19</td></td></td></td></td>	9.6 <td>45.7<td>21<td>28<td>AZ978966</td><td>AZ978966</td><td>2M0092B19</td></td></td></td>	45.7 <td>21<td>28<td>AZ978966</td><td>AZ978966</td><td>2M0092B19</td></td></td>	21 <td>28<td>AZ978966</td><td>AZ978966</td><td>2M0092B19</td></td>	28 <td>AZ978966</td> <td>AZ978966</td> <td>2M0092B19</td>	AZ978966	AZ978966	2M0092B19
18 <td>9.4<td>44.8</td><td>19<td>28<td>AZ655467</td><td>AZ655467</td><td>2M0255D04</td></td></td></td>	9.4 <td>44.8</td> <td>19<td>28<td>AZ655467</td><td>AZ655467</td><td>2M0255D04</td></td></td>	44.8	19 <td>28<td>AZ655467</td><td>AZ655467</td><td>2M0255D04</td></td>	28 <td>AZ655467</td> <td>AZ655467</td> <td>2M0255D04</td>	AZ655467	AZ655467	2M0255D04
19 <td>9.4<td>44.8</td><td>20<td>28<td>AZ359918</td><td>AZ359918</td><td>IM0530017</td></td></td></td>	9.4 <td>44.8</td> <td>20<td>28<td>AZ359918</td><td>AZ359918</td><td>IM0530017</td></td></td>	44.8	20 <td>28<td>AZ359918</td><td>AZ359918</td><td>IM0530017</td></td>	28 <td>AZ359918</td> <td>AZ359918</td> <td>IM0530017</td>	AZ359918	AZ359918	IM0530017
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21 <td>9.4<td>44.8</td><td>20<td>28<td>AZ579532</td><td>AZ579532</td><td>IM0224G12</td></td></td></td>	9.4 <td>44.8</td> <td>20<td>28<td>AZ579532</td><td>AZ579532</td><td>IM0224G12</td></td></td>	44.8	20 <td>28<td>AZ579532</td><td>AZ579532</td><td>IM0224G12</td></td>	28 <td>AZ579532</td> <td>AZ579532</td> <td>IM0224G12</td>	AZ579532	AZ579532	IM0224G12
22 <td>9.4<td>44.8</td><td>21<td>28<td>AZ387199</td><td>AZ387199</td><td>IM0367H10</td></td></td></td>	9.4 <td>44.8</td> <td>21<td>28<td>AZ387199</td><td>AZ387199</td><td>IM0367H10</td></td></td>	44.8	21 <td>28<td>AZ387199</td><td>AZ387199</td><td>IM0367H10</td></td>	28 <td>AZ387199</td> <td>AZ387199</td> <td>IM0367H10</td>	AZ387199	AZ387199	IM0367H10
23 <td>9.2<td>43.8</td><td>19<td>28<td>AZ458806</td><td>AZ458806</td><td>IM0146P20</td></td></td></td>	9.2 <td>43.8</td> <td>19<td>28<td>AZ458806</td><td>AZ458806</td><td>IM0146P20</td></td></td>	43.8	19 <td>28<td>AZ458806</td><td>AZ458806</td><td>IM0146P20</td></td>	28 <td>AZ458806</td> <td>AZ458806</td> <td>IM0146P20</td>	AZ458806	AZ458806	IM0146P20
24 <td>9.2<td>43.8</td><td>19<td>28<td>AZ816318</td><td>AZ816318</td><td>2M0085E05</td></td></td></td>	9.2 <td>43.8</td> <td>19<td>28<td>AZ816318</td><td>AZ816318</td><td>2M0085E05</td></td></td>	43.8	19 <td>28<td>AZ816318</td><td>AZ816318</td><td>2M0085E05</td></td>	28 <td>AZ816318</td> <td>AZ816318</td> <td>2M0085E05</td>	AZ816318	AZ816318	2M0085E05
25 <td>9.2<td>43.8</td><td>21<td>28<td>AZ648575</td><td>AZ648575</td><td>IM0517G07</td></td></td></td>	9.2 <td>43.8</td> <td>21<td>28<td>AZ648575</td><td>AZ648575</td><td>IM0517G07</td></td></td>	43.8	21 <td>28<td>AZ648575</td><td>AZ648575</td><td>IM0517G07</td></td>	28 <td>AZ648575</td> <td>AZ648575</td> <td>IM0517G07</td>	AZ648575	AZ648575	IM0517G07
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27 <td>9.2<td>42.9</td><td>19<td>28<td>AZ330741</td><td>AZ330741</td><td>IM0056G11</td></td></td></td>	9.2 <td>42.9</td> <td>19<td>28<td>AZ330741</td><td>AZ330741</td><td>IM0056G11</td></td></td>	42.9	19 <td>28<td>AZ330741</td><td>AZ330741</td><td>IM0056G11</td></td>	28 <td>AZ330741</td> <td>AZ330741</td> <td>IM0056G11</td>	AZ330741	AZ330741	IM0056G11
28 <td>9.2<td>42.9</td><td>19<td>28<td>AZ457990</td><td>AZ457990</td><td>IM0261E11</td></td></td></td>	9.2 <td>42.9</td> <td>19<td>28<td>AZ457990</td><td>AZ457990</td><td>IM0261E11</td></td></td>	42.9	19 <td>28<td>AZ457990</td><td>AZ457990</td><td>IM0261E11</td></td>	28 <td>AZ457990</td> <td>AZ457990</td> <td>IM0261E11</td>	AZ457990	AZ457990	IM0261E11
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30 <td>9.2<td>42.9</td><td>20<td>28<td>AZ784073</td><td>AZ784073</td><td>2M0026B06</td></td></td></td>	9.2 <td>42.9</td> <td>20<td>28<td>AZ784073</td><td>AZ784073</td><td>2M0026B06</td></td></td>	42.9	20 <td>28<td>AZ784073</td><td>AZ784073</td><td>2M0026B06</td></td>	28 <td>AZ784073</td> <td>AZ784073</td> <td>2M0026B06</td>	AZ784073	AZ784073	2M0026B06
31 <td>9.2<td>42.9</td><td>20<td>29<td>TA158A03P</td><td>TA158A03P</td><td></td></td></td></td>	9.2 <td>42.9</td> <td>20<td>29<td>TA158A03P</td><td>TA158A03P</td><td></td></td></td>	42.9	20 <td>29<td>TA158A03P</td><td>TA158A03P</td><td></td></td>	29 <td>TA158A03P</td> <td>TA158A03P</td> <td></td>	TA158A03P	TA158A03P	
32 <td>9.2<td>42.9</td><td>21<td>28<td>AZ435931</td><td>AZ435931</td><td>IM0223L15</td></td></td></td>	9.2 <td>42.9</td> <td>21<td>28<td>AZ435931</td><td>AZ435931</td><td>IM0223L15</td></td></td>	42.9	21 <td>28<td>AZ435931</td><td>AZ435931</td><td>IM0223L15</td></td>	28 <td>AZ435931</td> <td>AZ435931</td> <td>IM0223L15</td>	AZ435931	AZ435931	IM0223L15
33 <td>8.8<td>41.9</td><td>19<td>28<td>AZ413661</td><td>AZ413661</td><td>IM0197I07</td></td></td></td>	8.8 <td>41.9</td> <td>19<td>28<td>AZ413661</td><td>AZ413661</td><td>IM0197I07</td></td></td>	41.9	19 <td>28<td>AZ413661</td><td>AZ413661</td><td>IM0197I07</td></td>	28 <td>AZ413661</td> <td>AZ413661</td> <td>IM0197I07</td>	AZ413661	AZ413661	IM0197I07
34 <td>8.8<td>41.9</td><td>19<td>28<td>AZ446372</td><td>AZ446372</td><td>IM0242P18</td></td></td></td>	8.8 <td>41.9</td> <td>19<td>28<td>AZ446372</td><td>AZ446372</td><td>IM0242P18</td></td></td>	41.9	19 <td>28<td>AZ446372</td><td>AZ446372</td><td>IM0242P18</td></td>	28 <td>AZ446372</td> <td>AZ446372</td> <td>IM0242P18</td>	AZ446372	AZ446372	IM0242P18
35 <td>8.8<td>41.9</td><td>19<td>28<td>AZ447197</td><td>AZ447197</td><td>IM0244A08</td></td></td></td>	8.8 <td>41.9</td> <td>19<td>28<td>AZ447197</td><td>AZ447197</td><td>IM0244A08</td></td></td>	41.9	19 <td>28<td>AZ447197</td><td>AZ447197</td><td>IM0244A08</td></td>	28 <td>AZ447197</td> <td>AZ447197</td> <td>IM0244A08</td>	AZ447197	AZ447197	IM0244A08
36 <td>8.8<td>41.9</td><td>20<td>13<td>B0583464</td><td>B0583464</td><td>E011979-0</td></td></td></td>	8.8 <td>41.9</td> <td>20<td>13<td>B0583464</td><td>B0583464</td><td>E011979-0</td></td></td>	41.9	20 <td>13<td>B0583464</td><td>B0583464</td><td>E011979-0</td></td>	13 <td>B0583464</td> <td>B0583464</td> <td>E011979-0</td>	B0583464	B0583464	E011979-0
37 <td>8.8<td>41.9</td><td>20</td><td>28<td>AZ308291</td><td>AZ308291</td><td>IM0011E10</td></td></td>	8.8 <td>41.9</td> <td>20</td> <td>28<td>AZ308291</td><td>AZ308291</td><td>IM0011E10</td></td>	41.9	20	28 <td>AZ308291</td> <td>AZ308291</td> <td>IM0011E10</td>	AZ308291	AZ308291	IM0011E10
38 <td>8.8<td>41.9</td><td>21<td>28<td>AZ394677</td><td>AZ394677</td><td>IM0158A24</td></td></td></td>	8.8 <td>41.9</td> <td>21<td>28<td>AZ394677</td><td>AZ394677</td><td>IM0158A24</td></td></td>	41.9	21 <td>28<td>AZ394677</td><td>AZ394677</td><td>IM0158A24</td></td>	28 <td>AZ394677</td> <td>AZ394677</td> <td>IM0158A24</td>	AZ394677	AZ394677	IM0158A24
39 <td>8.8<td>41.9</td><td>21<td>28<td>AZ972047</td><td>AZ972047</td><td>2M0245F16</td></td></td></td>	8.8 <td>41.9</td> <td>21<td>28<td>AZ972047</td><td>AZ972047</td><td>2M0245F16</td></td></td>	41.9	21 <td>28<td>AZ972047</td><td>AZ972047</td><td>2M0245F16</td></td>	28 <td>AZ972047</td> <td>AZ972047</td> <td>2M0245F16</td>	AZ972047	AZ972047	2M0245F16
40 <td>8.6<td>41.0</td><td>16<td>9<td>AI075064</td><td>AI075064</td><td>ou61g11.x</td></td></td></td>	8.6 <td>41.0</td> <td>16<td>9<td>AI075064</td><td>AI075064</td><td>ou61g11.x</td></td></td>	41.0	16 <td>9<td>AI075064</td><td>AI075064</td><td>ou61g11.x</td></td>	9 <td>AI075064</td> <td>AI075064</td> <td>ou61g11.x</td>	AI075064	AI075064	ou61g11.x
41 <td>8.6<td>41.0</td><td>19<td>9<td>AI360784</td><td>AI360784</td><td>qx98g07.x</td></td></td></td>	8.6 <td>41.0</td> <td>19<td>9<td>AI360784</td><td>AI360784</td><td>qx98g07.x</td></td></td>	41.0	19 <td>9<td>AI360784</td><td>AI360784</td><td>qx98g07.x</td></td>	9 <td>AI360784</td> <td>AI360784</td> <td>qx98g07.x</td>	AI360784	AI360784	qx98g07.x
42 <td>8.6<td>41.0</td><td>19<td>28<td>AZ386856</td><td>AZ386856</td><td>IM0101K12</td></td></td></td>	8.6 <td>41.0</td> <td>19<td>28<td>AZ386856</td><td>AZ386856</td><td>IM0101K12</td></td></td>	41.0	19 <td>28<td>AZ386856</td><td>AZ386856</td><td>IM0101K12</td></td>	28 <td>AZ386856</td> <td>AZ386856</td> <td>IM0101K12</td>	AZ386856	AZ386856	IM0101K12
43 <td>8.6<td>41.0</td><td>19<td>28<td>AZ438791</td><td>AZ438791</td><td>IM0229K01</td></td></td></td>	8.6 <td>41.0</td> <td>19<td>28<td>AZ438791</td><td>AZ438791</td><td>IM0229K01</td></td></td>	41.0	19 <td>28<td>AZ438791</td><td>AZ438791</td><td>IM0229K01</td></td>	28 <td>AZ438791</td> <td>AZ438791</td> <td>IM0229K01</td>	AZ438791	AZ438791	IM0229K01
44 <td>8.6<td>41.0</td><td>19<td>28<td>AZ485378</td><td>AZ485378</td><td>IM0312F16</td></td></td></td>	8.6 <td>41.0</td> <td>19<td>28<td>AZ485378</td><td>AZ485378</td><td>IM0312F16</td></td></td>	41.0	19 <td>28<td>AZ485378</td><td>AZ485378</td><td>IM0312F16</td></td>	28 <td>AZ485378</td> <td>AZ485378</td> <td>IM0312F16</td>	AZ485378	AZ485378	IM0312F16
45 <td>8.6<td>41.0</td><td>19<td>28<td>AZ485378</td><td>AZ485378</td><td>IM0312F16</td></td></td></td>	8.6 <td>41.0</td> <td>19<td>28<td>AZ485378</td><td>AZ485378</td><td>IM0312F16</td></td></td>	41.0	19 <td>28<td>AZ485378</td><td>AZ485378</td><td>IM0312F16</td></td>	28 <td>AZ485378</td> <td>AZ485378</td> <td>IM0312F16</td>	AZ485378	AZ485378	IM0312F16

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0042 row: N column: 20
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

1. 21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0042N20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 0 c 14 g 0 t
 ORIGIN

Query Match 57.1%; Score 12; DB 28; Length 21;
 Best Local Similarity 75.0%; Pred. No. 5.1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCATCCTCACCTTGCTCCTC 20
 |||||
 Db 21 TCCTCCTCCTCCTCCTCCTC 2

RESULT 2

AZ775540/c 19 bp DNA linear GSS 16-FEB-2001
 LOCUS
 DEFINITION 2M0008H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0008H15 F, genomic survey sequence.

ACCESSION AZ775540
 VERSION AZ775540.1 GI:12902183
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

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 Insert Length: 10000 Std Error: 0.00
 Plate: 0008 row: H column: 15
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

1. 19
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0008H15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 0 c 12 g 0 t
 ORIGIN

Query Match 52.4%; Score 11; DB 28; Length 19;
 Best Local Similarity 73.7%; Pred. No. 1.2e+06;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCATCCTCACCTTGCTCCTC 19
 |||||
 Db 19 TCCTCCTCCTCCTCCTCCTC 1

RESULT 3

AZ829601 20 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0107D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0107D03 R, genomic survey sequence.

ACCESSION AZ829601
 VERSION AZ829601.1 GI:12999605
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

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 Insert Length: 10000 Std Error: 0.00
 Plate: 0107 row: D column: 03
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES

Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0107D03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 7 a 7 c 0 g 6 t

ORIGIN

Query Match 49.5%; Score 10.4; DB 28; Length 20;
 Best Local Similarity 70.0%; Pred. No. 2e+06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CATCTCATCCCTTGCTCTCA 21
 |||||
 Db 1 CATCATCATCATCATCA 20

RESULT 4

AZ580960
 LOCUS AZ580960 21 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0369P04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369P04 R, genomic survey sequence.

ACCESSION AZ580960
 VERSION AZ580960.1 GI:11695495
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

UNPUBLISHED
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84112, USA
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 Insert Length: 10000 Std Error: 0.00
 Plate: 0369 row: P column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0369P04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 2 a 9 c 2 g 8 t

ORIGIN

Query Match 49.5%; Score 10.4; DB 28; Length 21;
 Best Local Similarity 91.7%; Pred. No. 2e+06;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CACCTCTGCTCT 19
 |||||
 Db 8 CACCTCTGCTCT 19

RESULT 5

AZ313243
 LOCUS AZ313243 21 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M029H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0029H16 R, genomic survey sequence.

ACCESSION AZ313243
 VERSION AZ313243.1 GI:10357979
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

UNPUBLISHED
 CONTACT: Robert B. Weiss
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 Insert Length: 10000 Std Error: 0.00
 Plate: 0029 row: H column: 16
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

source

1. .21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0029H16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 0 c 13 g 6 t
 ORIGIN
 Query Match 47.6%; Score 10; DB 28; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.8e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATCCTCACCC 12

Db 21 ATCCTCACCC 12

RESULT 6
 AZ849030/c 21 bp DNA linear GSS 21-FEB-2001
 LOCUS 2M0150117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0150117 F, genomic survey sequence.

ACCESSION AZ849030

VERSION AZ849030.1 GI:13032696

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, N., Ross, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished

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 Insert Length: 10000 Std Error: 0.00
 Plate: 0150 row: I column: 17
 Seq primer: CGTTGTAACACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

source

1. .21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0150117"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 0 c 15 g 0 t

ORIGIN

Query Match 47.6%; Score 10; DB 28; Length 21;
 Best Local Similarity 72.2%; Pred. No. 2.8e+06;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCATCCTCACCCCTGTCC 18

Db 18 TCCTCCTCTCCTCCCC 1

RESULT 7

BG926067

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

BG926067 13 bp mRNA linear EST 06-NOV-2001
 HNC23-1-B8-R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
 sequence.
 BG926067
 BG926067.1 GI:14320590
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 13)
 Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.
 Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 21482651

PUBMED
COMMENT

11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@sk.com
Seq primer: T7.

FEATURES

source

1. .13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 0 a 9 c 0 g 4 t

ORIGIN

Query Match 46.7%; Score 9.8; DB 12; Length 13;
Best Local Similarity 84.6%; Pred. No. 3e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCACCCCTTGTC 18

Db 1 CTCACCCCTTGTC 13

RESULT 8

AZ654730

LOCUS

DEFINITION AZ654730 21 bp DNA linear GSS 14-DEC-2000
IM0529P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529P05 F, genomic survey sequence.

ACCESSION AZ654730

VERSION AZ654730.1 GI:11791876

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0529 row: P column: 05

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES

source

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529P05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 4 a 13 c 0 g 4 t

ORIGIN

Query Match 46.7%; Score 9.8; DB 28; Length 21;
Best Local Similarity 84.6%; Pred. No. 3.4e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCTCACCCCTT 14

Db 9 CATCCCCCACCCCT 21

RESULT 9

AZ657586

LOCUS

DEFINITION AZ657586 21 bp DNA linear GSS 14-DEC-2000
IM0533D24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0533D24 R, genomic survey sequence.

ACCESSION AZ657586

VERSION AZ657586.1 GI:11794732

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0533 row: D column: 24

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES

source

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0533D24"
/sex="Male"

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      2 a      10 c      2 g      7 t
ORIGIN

```

```

Query Match      46.7%; Score 9.8; DB 28; Length 21;
Best Local Similarity 84.6%; Pred. No. 3.4e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 5 CCTCACCCTTCTC 17
    |||||
Db 3 CCTCTCCCTTCTC 15

```

```

RESULT 10
A2785825      21 bp      DNA      linear      GSS 16-FEB-2001
LOCUS      2M0030G05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION      clone UUGC2M0030G05 R, genomic survey sequence.
ACCESSION      A2785825
VERSION      A2785825.1 GI:12922972
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0030 row: G column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0030G05"

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FEATURES
source

```

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      6 a      8 c      3 g      4 t
ORIGIN

```

```

Query Match      46.7%; Score 9.8; DB 28; Length 21;
Best Local Similarity 84.6%; Pred. No. 3.4e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 TCATCTCACCCT 13
    |||||
Db 6 TCGCCTCACCCT 18

```

```

RESULT 11
A1696833/c    19 bp      mRNA      linear      EST 17-DEC-1999
LOCUS      WC74e09.x1 NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2324392 3'
DEFINITION      similar to TR:Q01942 Q01942 EXTENSIN ;contains element TAR1
ACCESSION      A1696833
VERSION      A1696833.1 GI:4984733
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-1@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

```

```

ACCESSION      A1696833
VERSION      A1696833.1 GI:4984733
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-1@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

```

```

Trace considered overall poor quality
Insert Length: 1542 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2324392"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Panl"

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```

FEATURES
source

```

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site.1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

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BASE COUNT      4 a      1 c      14 g      0 t
ORIGIN
Query Match      45.7%; Score 9.6; DB 9; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.9e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CCTCACCCCTTGTCTCT 20
    ||||| ||| |||||
Db 19 CCTCCCCCTCTCTCTC 4

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```

RESULT 12
AZ432757/c
LOCUS      AZ432757      19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION IM0218L14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0218L14 F, genomic survey sequence.
ACCESSION  AZ432757
VERSION     AZ432757.1 GI:10556770
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0218 row: L column: 14
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0218L14"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number was ligated
inducible derivative of plasmid RI. The vector was ligated

```

with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

BASE COUNT      6 a      0 c      13 g      0 t
ORIGIN
Query Match      45.7%; Score 9.6; DB 28; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.9e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CCTCACCCCTTGTCTCT 20
    ||||| ||| |||||
Db 19 CCTCTCCTCTCTCTCTC 4

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```

RESULT 13
AZ654214/c
LOCUS      AZ654214      19 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION IM0528H13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0528H13 F, genomic survey sequence.
ACCESSION  AZ654214
VERSION     AZ654214.1 GI:11791360
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0528 row: H column: 13
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0528H13"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

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FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0218L14"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 0 c 14 g 1 t

ORIGIN

Query Match 45.7%; Score 9.6; DB 28; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.9e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CCTCACCCCTTGCTCTC 20

Db 19 CCTCCCTACCCCTC 4

RESULT 14

AZ941399

LOCUS

DEFINITION 2M0201F07F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0201F07 F, genomic survey sequence.

ACCESSION AZ941399

VERSION AZ941399.1

KEYWORDS GI:13803898

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0201 row: F column: 07

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0201F07"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydronically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 7 c 0 g 8 t

ORIGIN

Query Match 45.7%; Score 9.6; DB 28; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.9e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CATCCTCACCCCTTGTC 17

Db 2 CATCTATCCCTTCTC 17

RESULT 15

AZ832404/c

LOCUS

DEFINITION 2M0112J16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112J16 R, genomic survey sequence.

ACCESSION AZ832404

VERSION AZ832404.1

KEYWORDS GI:13002312

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

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plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: J column: 16

Seq primer: CACACGGAACGACGATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0112J16"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydronically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 2 c 7 g 7 t
ORIGIN

Query Match 45.7%; Score 9.6; DB 28; Length 20;
Best Local Similarity 75.0%; Pred. No. 4e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTCACCCCTTGTCTCTCA 21
| | | | | | |
Db 20 CACACACTTGTCTCAC 5

Search completed: February 20, 2004, 02:39:19
Job time : 1494 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 00:42:09 ; Search time 45.5 Seconds
(without alignments)
203.715 Million cell updates/sec

Title: US-10-085-108-21_COPY_175_195
Perfect score: 21
Sequence: 1 TCATCCTCACCCCTGTCTCTCA 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 352324

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	75.2	20	3	US-09-433-699-31
2	14	66.7	20	3	US-09-226-012-47
3	13.8	65.7	20	1	US-08-317-432A-26
4	13.4	65.7	21	1	US-08-317-432A-27
5	13.4	63.8	21	4	US-09-422-978-10433
6	12.8	61.0	20	3	US-09-429-323-46
7	12.8	61.0	20	4	US-09-702-327-63
8	12.8	61.0	21	4	US-09-422-978-9636
9	12.6	60.0	20	3	US-09-433-699-40
10	12.6	60.0	20	4	US-09-622-277-2
11	12.6	60.0	21	4	US-09-380-836-88
12	12.4	59.0	18	3	US-09-630-706-59
13	12.4	59.0	19	2	US-08-359-705B-22
14	12.4	59.0	19	2	US-08-286-846A-22
15	12.4	59.0	19	2	US-08-457-860A-22
16	12.4	59.0	19	3	US-08-444-622A-22
17	12.4	59.0	19	3	US-08-942-562-22
18	12.4	59.0	19	3	US-09-156-923-22
19	12.4	59.0	21	4	US-09-380-836-90
20	12.2	58.1	17	4	US-09-371-772B-4357
21	12.2	58.1	18	1	US-08-161-673A-5
22	12.2	58.1	18	2	US-08-481-876-5
23	12.2	58.1	18	3	US-09-185-437-5
24	12.2	58.1	18	3	US-08-652-425-3
25	12.2	58.1	18	3	US-09-632-580A-86
26	12.2	58.1	18	4	US-09-422-978-11706
27	12.2	58.1	20	2	US-08-810-599-47

Sequence 38, Appl
Sequence 38, Appl
Sequence 44, Appl
Sequence 39, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 4, Appl
Sequence 59, Appl
Sequence 64, Appl
Sequence 70, Appl
Sequence 83, Appl
Sequence 5, Appl
Sequence 9, Appl
Sequence 53, Appl
Sequence 53, Appl

US-08-866-340-38
US-08-757-438-38
US-09-103-875-44
US-09-302-681-39
PCT-US93-09232-2
US-07-947-683-6
US-08-400-323-10
US-08-533-996A-4
US-08-863-639A-59
US-08-863-639A-64
US-08-863-639A-70
US-08-863-639A-83
US-08-486-343A-5
PCT-US95-07349-5
US-08-098-942C-9
US-08-219-842-53
US-08-219-842-86
US-08-451-096-53

ALIGNMENTS

RESULT 1
US-09-433-699-31
; Sequence 31, Application US/09433699B
; Patent No. 6165786
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cosset
; TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
; FILE REFERENCE: RTS-0109
; CURRENT APPLICATION NUMBER: US/09/433.699B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-433-699-31

Query Match 75.2%; Score 15.8; DB 3; Length 20;
Best Local Similarity .89.5%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCATCCTCACCCCTGTCTCT 19
Db 2 TCATCCTCACCCCTGTCTCT 20

RESULT 2
US-09-226-012-47/C
; Sequence 47, Application US/09226012
; Patent No. 6207383
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; TITLE OF INVENTION: SYNDROME GENE
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226.012
; CURRENT FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122.847
; EARLIER FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-226-012-47

Query Match 66.7%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCACCCCTTGCTCA 18
DB 16 CCTCACCCCTTGCTCA 3

RESULT 3
US-08-317-432A-26
; Sequence 26, Application US/08317432A
; Patent No. 5710028
; GENERAL INFORMATION:
; APPLICANT: Nurit Eyal and Nir Navot
; TITLE OF INVENTION: A method of quick screening and
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
; STREET: 2940 Birchtree lane
; CITY: Silver Spring
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 20906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,432A
; FILING DATE: 4-Oct-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/919,872
; FILING DATE: 27-Jul-92
; APPLICATION NUMBER: 08/084,505
; FILING DATE: 1-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 128/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-317-432A-27

Query Match 65.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1e+03; Indels 2; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTCACCCCTTGCTCA 21
DB 2 CCTCACCCCTTGCTCA 18

RESULT 4
US-08-317-432A-27/c
; Sequence 27, Application US/08317432A
; Patent No. 5710028
; GENERAL INFORMATION:
; APPLICANT: Nurit Eyal and Nir Navot
; TITLE OF INVENTION: A method of quick screening and

; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
; STREET: 2940 Birchtree lane
; CITY: Silver Spring
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 20906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,432A
; FILING DATE: 4-Oct-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/919,872
; FILING DATE: 27-Jul-92
; APPLICATION NUMBER: 08/084,505
; FILING DATE: 1-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 128/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-317-432A-27

Query Match 65.7%; Score 13.8; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 1e+03; Indels 2; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTCACCCCTTGCTCA 21
DB 20 CCTCACCCCTTGCTCA 4

RESULT 5
US-09-422-978-10433
; Sequence 10433, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10433
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:

; NAME/KEY: primer bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-11851 for SEQ 2568, in complement
US-09-422-978-10433

Query Match 63.8%; Score 13.4; DB 4; Length 21;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCACCCCTTGCTCTC 20
|||||
Db 7 CTCACCTTGCTCTC 21

RESULT 6
US-09-429-323-46
; Sequence 46, Application US/09429323A
; Patent No. 6140126
; Patent No. 6140126 6140123
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF Y-BOX BINDING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0092
; CURRENT APPLICATION NUMBER: US/09/429,323A
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-429-323-46

Query Match 61.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCTCACCCCTTGTC 17
|||||
Db 2 CCTCCTCACCCCTTTC 17

RESULT 7
US-09-702-327-63
; Sequence 63, Application US/09702327
; Patent No. 6426220
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION
; FILE REFERENCE: RTS-0097
; CURRENT APPLICATION NUMBER: US/09/702,327
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-327-63

Query Match 61.0%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCACCCCTTGCTCTCA 21
|||||
Db 1 CTCATCTTGCTCTCA 16

RESULT 8
US-09-422-978-9636/c
; Sequence 9636, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET-020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9636
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-6261 for SEQ 1771, in complement
US-09-422-978-9636

Query Match 61.0%; Score 12.8; DB 4; Length 21;
Best Local Similarity 87.5%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTCACCCCTTGCTCTC 20
|||||
Db 21 CCTCACCCCTTCTTC 6

RESULT 9
US-09-433-699-40
; Sequence 40, Application US/09433699B
; Patent No. 6165786
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
; FILE REFERENCE: RTS-0109
; CURRENT APPLICATION NUMBER: US/09/433,699B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-433-699-40

Query Match 60.0%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCATCCTCACCCCTTGCTCT 19
|||||
Db 1 TCATCCTCAGCCAGCTTCT 19

RESULT 10
US-09-622-277-2
; Sequence 2, Application US/09622277
; Patent No. 6521407
; GENERAL INFORMATION:
; APPLICANT: Warenius, Hilmar Meek

APPLICANT: Seabra, Laurence Anthony
TITLE OF INVENTION: METHODS FOR DETERMINING CHEMOSENSITIVITY OF CANCER CELLS BASED UP
FILE REFERENCE: 1417-188
CURRENT APPLICATION NUMBER: US/09/622,277
CURRENT FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: PCT/GB99/00500
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: GB 9903035.5
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: GB 9814545.1
PRIOR FILING DATE: 1998-07-03
PRIOR APPLICATION NUMBER: GB 9812151.0
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: GB 9803447.3
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: GB 9803446.5
PRIOR FILING DATE: 1998-02-18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR and DNA sequencing primer for exon 2/3 antisense
US-09-622-277-2

Query Match 60.8%; Score 12.6; DB 4; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATCCCTCACCCCTGTGCTCA 21
DB 1 AGCCACACCCCTGTGCTCA 19

RESULT 11
US-09-836-88/c
Sequence 88, Application US/09380836
Patent No. 6551775
GENERAL INFORMATION:
APPLICANT: Lifton, Richard P.
APPLICANT: Chang, Sue S.
APPLICANT: Rossier, Bernard C.
TITLE OF INVENTION: Method to Diagnose and Treat Pathological Conditions
TITLE OF INVENTION: Resulting from Deficient Ion Transport such as
TITLE OF INVENTION: Pseudohypoaldosteronism Type-1
FILE REFERENCE: 44574-5018-US
CURRENT APPLICATION NUMBER: US/09/380,836
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/040,171
PRIOR FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: PCT/US98/04661
PRIOR FILING DATE: 1998-03-11
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 88
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: G-6 forward
US-09-380-836-88

Query Match 60.0%; Score 12.6; DB 4; Length 21;
Best Local Similarity 78.9%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATCCTCACCCCTGTGCTC 20
DB 19 CACACTCAGCCCTGTGCTC 1

RESULT 12
US-09-630-706-59
Sequence 59, Application US/09630706
Patent No. 6277640
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
FILE REFERENCE: RTS-0053
CURRENT APPLICATION NUMBER: US/09/630,706
CURRENT FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 59
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-630-706-59

Query Match 59.0%; Score 12.4; DB 3; Length 18;
Best Local Similarity 92.9%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CACCCCTGTGCTCA 21
DB 2 CACTCTGTGCTCA 15

RESULT 13
US-08-359-705B-22/c
Sequence 22, Application US/08359705B
Patent No. 5844092
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Shelton, David L.
APPLICANT: Urfer, Roman
TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/359,705B
FILING DATE: 20-Dec-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286846
FILING DATE: 08/10/94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/215139
FILING DATE: 03/18/94
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0873P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs

; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-359-705B-22

Query Match 59.0%; Score 12.4; DB 2; Length 19;
Best Local Similarity 92.9%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCACCCCTTGCTCT 19
| | | | | | | | | | | | | | | | | | | | |
Db 19 CTCACCCCTTGCCCT 6

RESULT 14

US-08-286-846A-22/c
; Sequence 22, Application US/08286846A
; Patent No. 5877016
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; APPLICANT: Urfer, Roman
; TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,846A
; FILING DATE: 05-Aug-1994

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P0873P1
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-286-846A-22

Query Match 59.0%; Score 12.4; DB 2; Length 19;
Best Local Similarity 92.9%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCACCCCTTGCTCT 19
| | | | | | | | | | | | | | | | | | | | |
Db 19 CTCACCCCTTGCCCT 6

RESULT 15

US-08-457-880A-22/c
; Sequence 22, Application US/08457880A
; Patent No. 5910574
; GENERAL INFORMATION:
; APPLICANT: Leonard G. Presta
; APPLICANT: David L. Shelton
; APPLICANT: Roman Urfer

; TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,880A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,622
; FILING DATE: 19-May-1995
; APPLICATION NUMBER: 08/286846
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P0873P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-457-880A-22

Query Match 59.0%; Score 12.4; DB 2; Length 19;
Best Local Similarity 92.9%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCACCCCTTGCTCT 19
| | | | | | | | | | | | | | | | | | | | |
Db 19 CTCACCCCTTGCCCT 6

Search completed: February 20, 2004, 02:40:58
Job time : 47.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 00:32:29 ; Search time 1490 Seconds
(without alignments)
342.546 Million cell updates/sec

Title: US-10-085-108-21_COPY_175_195

Perfect score: 21

Sequence: 1 TCATCCTCACCCCTTGCTCTCA 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 8380

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estmu:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_ham:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_ptg:*

27: em_gss_vrl:*

28: gb_gas1:*

29: gb_gas2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	57.1	21	28	AZ321746 1M0042N20
C 2	11	52.4	19	28	AZ775540 2M0008H15
C 3	10.4	49.5	20	28	AZ829601 2M0107D03
C 4	10.4	49.5	21	28	AZ580960 1M0369P04

C 5	10	47.6	21	28	AZ313243
C 6	10	47.6	21	28	AZ849030
C 7	9.8	46.7	13	12	BG926067 HNC23-1-E
C 8	9.8	46.7	21	28	AZ654730 1M0529P05
C 9	9.8	46.7	21	28	AZ657586 1M0533D24
C 10	9.8	46.7	21	28	AZ785825 2M0030G05
C 11	9.6	45.7	19	9	AI696833 wc74e09.x
C 12	9.6	45.7	19	28	AZ432757 1M0218L14
C 13	9.6	45.7	19	28	AZ654214 1M0528H13
C 14	9.6	45.7	19	28	AZ941399 2M0201F07
C 15	9.6	45.7	20	28	AZ832404 2M0112J16
C 16	9.6	45.7	21	28	AZ820567 2M0092B19
C 17	9.6	45.7	21	28	AZ978966 2M0255D04
C 18	9.4	44.8	19	28	AZ655467 1M0530O17
C 19	9.4	44.8	20	28	AZ359918 1M0103A01
C 20	9.4	44.8	20	28	AZ436762 1M0224G12
C 21	9.4	44.8	20	28	AZ579532 1M0367H10
C 22	9.4	44.8	21	28	AZ387199 1M0146P20
C 23	9.2	43.8	19	28	AZ458806 1M0263O12
C 24	9.2	43.8	19	28	AZ816318 2M0085E05
C 25	9.2	43.8	21	28	AZ648575 1M0517G07
C 26	9	42.9	19	9	AI648553 tz55e07.x
C 27	9	42.9	19	28	AZ330741 1M0056G11
C 28	9	42.9	19	28	AZ457990 1M0261R11
C 29	9	42.9	20	28	AZ307088 1M0008M23
C 30	9	42.9	20	28	AZ784073 2M0026B06
C 31	9	42.9	20	29	TA158A03P
C 32	9	42.9	21	28	AZ435931 1M0223L15
C 33	8.8	41.9	19	28	AZ413661 1M0197I07
C 34	8.8	41.9	19	28	AZ446372 1M0242F18
C 35	8.8	41.9	19	28	AZ447197 1M0244A08
C 36	8.8	41.9	20	13	BQ583464 E011979-0
C 37	8.8	41.9	20	28	AZ308291 1M0011B10
C 38	8.8	41.9	21	28	AZ394677 1M0158A24
C 39	8.8	41.9	21	28	AZ972047 2M0245F16
C 40	8.8	41.9	21	29	TA37H07P
C 41	8.6	41.0	16	9	AI075064 ou6g511.x
C 42	8.6	41.0	19	9	AI360784 qx98g07.x
C 43	8.6	41.0	19	28	AZ358656 1M0101K12
C 44	8.6	41.0	19	28	AZ438791 1M0229K01
C 45	8.6	41.0	19	28	AZ485378 1M0312F16

ALIGNMENTS

RESULT 1
AZ321746/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ321746
1M0042N20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0042N20 F, genomic survey sequence.
AZ321746
GI:10374795
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

Dunn, D., Royagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0042 row: N column: 20
 Seq primer: CGTTGTAACAGCAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

source

1. .21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0042N20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

7 a 0 C 14 g 0 t

Query Match 57.1%; Score 12; DB 28; Length 21;
 Best Local Similarity 75.0%; Pred. No. 5.1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCATCCTCACCTTGTCTC 20
 ||||| |||||
 Db 21 TCCTCCTCCTCCTCCTC 2

RESULT 2
 AZ775540/c

LOCUS AZ775540 19 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M00008H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0008H15 F, genomic survey sequence.

ACCESSION AZ775540

VERSION AZ775540.1 GI:12902183

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0008 row: H column: 15
 Seq primer: CGTTGTAACAGCAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0008H15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 0 C 12 g 0 t

Query Match 52.4%; Score 11; DB 28; Length 19;
 Best Local Similarity 73.7%; Pred. No. 1.2e+06;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCATCCTCACCTTGTCTC 19
 ||||| |||||
 Db 19 TCCTCCTCCTCCTCCTC 1

RESULT 3

AZ829601

LOCUS

DEFINITION

AZ829601 20 bp DNA linear GSS 20-FEB-2001

clone UUGC2M0107D03 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0107 row: D column: 03
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0107D03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 0 g 6 t
 ORIGIN
 Query Match 49.5%; Score 10.4; DB 28; Length 20;
 Best Local Similarity 70.0%; Pred. No. 2e+06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CATCTCTACCTTGCTCTCA 21
 DB 1 CATCATCATCATCATCA 20

RESULT 4

LOCUS AZ580960 21 bp DNA linear GSS 13-DEC-2000
 DEFINITION LM0369P04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369P04 R, genomic survey sequence.

ACCESSION AZ580960
 VERSION AZ580960.1 GI:11695495
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0369 row: P column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0369P04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 9 c 2 g 8 t
 ORIGIN
 Query Match 49.5%; Score 10.4; DB 28; Length 21;
 Best Local Similarity 91.7%; Pred. No. 2e+06;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CACCTTGCTCT 19
 DB 8 CACCTTGCTCT 19

RESULT 5

LOCUS AZ313243 21 bp DNA linear GSS 29-SEP-2000
 DEFINITION LM0029H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0029H16 R, genomic survey sequence.

ACCESSION AZ313243
 VERSION AZ313243.1 GI:10357979
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

University of Utah
Rm. 3068, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: gdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: 1 column: 17
Seq primer: CGTTGTAAACGACGCCGAGT
Class: plasmid ends
High quality sequence stop: 21.

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  /mol_type="genomic DNA"
  /strain="C57Bl/6J"
  /db_xref="taxon:10090"
  /clone="UUCG2M0150117"
  /sex="Male"
  /lab_hosts="E. Coli strain"
  /clone_libs="Mouse 10kb p
    /note="Vector: PWD42n;
    /musculus C57Bl/6J (male)
    Laboratory Mouse DNA Reso
    (http://www.jax.org/reso
    was hydrodynamically shea
    0.005 inch orifice at con
    was blunt end-repaired w
    A polynucleotide kinase. A
    ligated to the blunt end
    adapted DNA was purified
    10.5 kb range using prep
    electrophoresis. Vector
    of PWD42 [gi|4732114|gb|
    of inducible derivative of
    with adaptors complement
    purified. The sheared, an
    adapted vector DNA, an
    chemically-competent E.
    and selected for ampicil

```

BASE COUNT	6 a	0 c	15 g	0 t
ORIGIN				
Query Match	47.6%; Score 10; DB 28; Length 21;			
Best Local Similarity	72.2%; Prod. No. 2.8e+06;			

1 TCATCCTCACCCCTTGTC 18
||| ||| ||| |||
18 TCTCCTCTCCCTCCCC 1

[illegible]

sequence.
 BG926067
 VERSION
 BG926067.1 GI:14320590
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 13)
 Kumar, S., Connor, J.R., Dodds, R.A., Halsey W., Van Horn, M., Mao, J.,
 Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
 Lark, M.W.

Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651

PUBMED
COMMENT

11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: 17.

FEATURES

Location/Qualifiers

1. .13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 0 a 9 c 0 g 4 t

ORIGIN

Query Match 46.7%; Score 9.8; DB 12; Length 13;
Best Local Similarity 84.6%; Pred. No. 3e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCACCCCTTGTC 18

Db 1 CTCACCCCTTGTC 13

RESULT 8

AZ654730

LOCUS

DEFINITION AZ654730 21 bp DNA linear GSS 14-DEC-2000
1M0529P05F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0529P05 F, genomic survey sequence.

ACCESSION AZ654730

VERSION AZ654730.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0529 row: P column: 05

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

Location/Qualifiers

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0529P05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 4 a 13 c 0 g 4 t

ORIGIN

Query Match 46.7%; Score 9.8; DB 28; Length 21;
Best Local Similarity 84.6%; Pred. No. 3.4e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCTCACCCCTT 14

Db 9 CATCCCCACCCCT 21

RESULT 9

AZ657586

LOCUS

DEFINITION 1M0533D24R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0533D24 R, genomic survey sequence.

ACCESSION AZ657586

VERSION AZ657586.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0533 row: D column: 24

Seq primer: CACACAGGAACAGCTATGAC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

Location/Qualifiers

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0533D24"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 10 c 2 g 7 t
 ORIGIN

Query Match 46.7%; Score 9.8; DB 28; Length 21;
 Best Local Similarity 84.6%; Pred. No. 3.4e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTCACCCCTTGTCTC 17
 |||||
 Db 3 CCTCTCCCTTCTC 15

RESULT 10
 AZ785825
 LOCUS
 DEFINITION 2M0030G05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0030G05 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CONTACT: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0030 row: G column: 05
 Seq primer: CACACAGGACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES
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 1. .21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0030G05"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 8 c 3 g 4 t
 ORIGIN

Query Match 46.7%; Score 9.8; DB 28; Length 21;
 Best Local Similarity 84.6%; Pred. No. 3.4e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATCTCTCACCTT 13
 |||||
 Db 6 TCGCCCTCACCTT 18

RESULT 11
 AI696833/c
 LOCUS
 DEFINITION

AI696833 19 bp mRNA linear EST 17-DEC-1999
 wc74e09.x1 NCI_CGAP_Panl Homo sapiens cdna clone IMAGE:2324392 3', similar to TR:Q01942 Q01942 EXTENSIN ; contains element TARI

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Life Technologies catalog #: 11548-013
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1542 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source
 1. .19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2324392"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Panl"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site1: SalI; Site2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.72 kb. Life Technologies catalog #:

BASE COUNT 4 a 1 c 14 g 0 t
ORIGIN

Query Match 45.7%; Score 9.6; DB 9; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.9e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCTCACCCCTGTGCTTC 20
|||||
Db 19 CCTCCCCCCTGCTTC 4

RESULT 12
AZ432757/c
LOCUS
DEFINITION
IM0218114F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M021814 F, genomic survey sequence.

ACCESSION
AZ432757
VERSION
GSS.

KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0218 row: L column: 14

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M021814"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

BASE COUNT 6 a 0 c 13 g 0 t
ORIGIN

Query Match 45.7%; Score 9.6; DB 28; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.9e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCTCACCCCTGTGCTTC 20
|||||
Db 19 CCTCACCCCTGCTTC 4

RESULT 13

AZ654214/c

LOCUS

DEFINITION

1M0528H13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0528H13 F, genomic survey sequence.

ACCESSION
AZ654214

VERSION
GSS.

KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0528 row: H column: 13

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0528H13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 0 c 14 g 1 t

ORIGIN

Query Match 45.7%; Score 9.6; DB 28; Length 19;

Best Local Similarity 75.0%; Pred. No. 3.9e+06;

Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CCTCACCTTGCTCTC 20

Db 19 CCTCCCTACCCCTC 4

RESULT 14

AZ941399

DEFINITION 2M0201F07F Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0201F07 F, genomic survey sequence.

ACCESSION AZ941399

VERSION AZ941399.1 GI:13803898

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0201 row: F column: 07

Seq primer: CGTTGTAACGACGCCAGT

Class: Plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0201F07"

/sex="Female"

/lab host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 7 c 8 t

ORIGIN

Query Match 45.7%;

Best Local Similarity 75.0%; Pred. No. 3.9e+06;

Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CATCTCACCTTGCTC 17

Db 2 CATCTCACCTTGCTC 17

RESULT 15

AZ832404/c

LOCUS

DEFINITION 2M0112J16R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC2M0112J16 R, genomic survey sequence.

ACCESSION AZ832404

VERSION AZ832404.1 GI:13002312

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: J column: 16

Seq primer: CACACGGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

source

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0112J16"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g₁4732114[gb AFI29072.1], a copy-number inducible derivative of plasmid λ). The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT	4 a	2 c	7 g	7 t
ORIGIN				

```
Query Match      45.7%; Score 9.6; DB 28; Length 20;
Best Local Similarity 75.0%; Pred. No. 4e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 6 CTCACCCCTTGTCCTCA 21
DB 20 CACACACTTGTGCACA 5

Search completed: February 20, 2004, 02:39:19
Job time : 1494 secs

2. US-10-085-108-21' (1-1041)
 US-09-468-433C-2 Sequence 20, Application US/09468433C

Initial Score = 95	Optimized Score = 191	Significance = 2.26
Residue Identity = 33%	Matches = 213	Mismatches = 402
Gaps = 14	Conservative Substitutions = 0	

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|||||
TGGGAATCTGACGGATCGGAGG
X
10      20

450      460      470      480      490      500      510
AAGATCATCGGAAATAGTCCATTACTTTGATG-ACAGTCGTGAGATCTCTGCGTTTGTGACAGGCTC
|||||
CATTTGTGAGGCGCGCAATCAAGTTAGCGGGGGAAGAGTCTTAGACCTGGCCAGTCTCTAGGCTGAGGG
30      40      50      60      70      80      90
|||||
520      530      540      550      560      570      580
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|||||
CCCTGAGGAAGAACTCAGGGACCTCCACCATAGAGAGAAGAACCCCGSCCTGTACTGCGTCCGCTGAGA
100     110     120     130     140     150     160
|||||
590      600      610      620      630      640      650
GATTCACATTTTGGCAAGCATGCGCAAGTAGCTGTATCTCTCTTCACTGCTGGACTCTCATCCAAATCG
|||||
CTGGTAGTCCACAGCAGGGAATGCGCCACAGAGAAGGAGGAGGTGCGCGCCCTCTAGGGAAATAATAGG
170     180     190     200     210     220     230
|||||
660      670      680      690      700      710      720
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AAGACACTGAGGAGGG---CTGGGGGAACGCCCCACCTCAGAGGCGCAATCCCCAGAGATTCGCCACCTGC
240     250     260     270     280     290     300
|||||
730      740      750      760      770      780      790      800
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|||||
TCTCAAGTATCAGCCCTGTAGAGTCCCACTCAGCTCAGG---CGGGGTGGCAGCCATCTTATTCCTGG
310     320     330     340     350     360     370
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810      820      830      840      850      860      870

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950 960 970 980 990 1000 1010
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 530 540 550 560 570 580 590

1020 1030 1040
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 TCAGGATGTGGCGTTGCTCTGAGTTTTCCTTAGGCCAGCAGAGTGGTGGAGGCTGGCCCTCTCTGAG
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AAGCCGTGA
 670

3. US-10-085-108-21' (1-1041)
 US-09-501-104B-2 Sequence 20, Application US/09501104B

Initial Score = 95 . Optimized Score = 191 Significance = 2.26
 Residue Identity = 33% Matches = 213 Mismatches = 402
 Gaps = 14 Conservative Substitutions = 0

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 GAGTGTTCGGGGTCCATATCAGTCAGGCGAATGCCAAAATTAGCTCTATGAATCATGGCTTTCCCG
 TGGGAATCTGACCGATCGGAGG
 X 10 20

450 460 470 480 490 500 510
 AAGATCATGGGAAATAGTCTTATCTTTATGATG-ACAGTCGTGAGCATCTCGCTTTTGAGCAGGCTC
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 30 40 50 60 70 80 90

520 530 540 550 560 570 580
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 100 110 120 130 140 150 160

590 600 610 620 630 640 650
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660 670 680 690 700 710 720
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 240 250 260 270 280 290 300

730 740 750 760 770 780 790 800
 GATCTTGGGAGACCTCGGAGGAATCTCAGAGGACTCTCGGGAAGAGTGGCATCCAGCAGCAGGCAT
 TCCTCAAGTATCAGCCCTGTAGACTCCCACTCAGTCTCAG---CGGGTGGCAGCCATCTTATTCCTGG
 310 320 330 340 350 360 370

810 820 830 840 850 860 870
 ATCCTCATCTTCTGGAAACCCCGAATAGAGTAGAGGGTTAGGACAAGGGTGAAGGATGAGGACA

[illegible]

8. US-10-085-108-21' (1-1041)
US-09-501-104B-1 Sequence 10, Application US/09501104B

	Initial Score =	81	Optimized Score =	203	Significance =	1.79
Residue Identity =	3%	Matches =	215	Mismatches =	346	
Gaps	=	10	Conservative Substitutions	=	0	
430	440	450	460	470	x 480	490
ACTCATGGGCTTTCCCGAAGATCATGGGAAATAGTCCTTATCTTGTGACAGCTGCATCTGTG						
					TGGGAATCTGACGGATCGGAGG	
					X	10 20
500	510	520	530	540	550	560

9. US-10-085-108-21' (1-1041)
US-09-468-433C-2 Sequence 25, Application US/09468433C

Initial Score	=	67	Optimized Score	=	338	Significance	=	1.32
Residue Identity	=	36%	Matches	=	393	Mismatches	=	628
Gaps	=	42	Conservative Substitutions	=			=	0

X 10 20 30 40 50 60
 CTAGGATGATATCGATAGCT-----TGGATAAAACTCTAAGACTTCTTGTCTGGCGCTCTGTAAT
 ATGCCTCGGGGTCACAAGAGTAGCTTCGCTTCTGAGAAACGCCAGAGACCAATGGTCAGGCCACAGGGT
 X 10 20 30 40 50 60 70
 70 80 90 100 110 120 130
 GGGCTCTTGGACCCCAAAAAATCATACGTGAGAGAGCACTGTTGGCACTCCCGGTACTCCAGGTACT
 CTCACGGGTCCCAGGCCCACTGCAGAGAAGCAGGAAGAGTCCCACTTCTCCTCATCTCTTCTGGCGCTTGT
 80 90 100 110 120 130 140
 140 150 160 170 180 190 200
 TTCTCTGCACCCCAATGTATAGTGAGCAGCTTCTCGGATCCCCATATATAAGTGTCTCCCTCCGACGACACA

10. US-10-085-108-21' (1-1041)
US-09-501-104B-2 Sequence 25, Application US/09501104B

Initial Score = 67 Optimized Score = 338 Significance = 1.32
Residue Identity = 36% Matches = 393 Mismatches = 628
Gaps = 42 Conservative Substitutions = 0

X 10 20 30 40 50 60
CTAGGGATGATCTCTGGATAGCT-----TGGATAAAAACTTAAGACTTCTCTTGTCTGGCCTCTGAAT
ATGCCTCGGGGTCAAGAGTAAGCTCCGTACCTGTGAGAAAGCCACAGAGACCAATGGTCAGCCACACAGGCT
X 10 20 30 40 50 60 70
GGGCTTTGGACCCCAAAAAATTCAATAGCTGGAGGAGCACTTTTGGGCACCTCCCGGTATCTCCAGTACT
CTCAGGGTCCCGAGGCCACTGCAGAGACGAAAGAGTCCCACTCTCTCTCATCTCTCTCTCTCGCGCTTCT
X 80 90 100 110 120 130 140
TTCTCTGCACCAATGATAGTAGAGCAGCTTTCTGGATGCCCATATATAAGTGTCTCCCTCCAGCACACA
CTGGGTG-----ATTGTCGTAGGTCTTCTGATGCTCAATTCCTCAGAGTCTCAGGGAGTGTCCAC
150 160 170 180 190 200
210 220 230 240 250 260 270
CCCTATTGGCACTCAACATTTCCAGAGACCTCTCTGGGGACACAGTGCCTTTATGAAGATCACTACTGA
CACTGGGTCTCTGATGAGTGTGTTTCATATTCAAAATCCGATGTGGTGCACCGCCAAAGGCAAGATGAGA-AAA
280 290 300 310 320 330 340
GTCCAAGCACCTCCCGTGATGCCCTCCG--TTCTCTCAGAGTCTCAGGGAGCTTCAACCACTGGCTCTCTCTGA
280 290 300 310 320 330 340
ATGTCTCTCAAGAAATAGAGTGGTTGTGCGGGTCCATATCAGTCAGGCAATGCCAAAAATTAGCTCTTA
TCAGAGTCTTCAGGCTCAAAATATGATGTGGTGCACCGCCAGGATGAGAAAGTCCAAGCACTTCCCA
350 360 370 380 390 400 410
TCAATCATATGGCTTTCCGAAGATCATGAGGAAAAATGTCCTTATCTTGTGATGAGTCAGTCGTGAGACTCT
TCATGTCTCCGTTCTCAGAGTCTCAGGAGCTTCACCCACTGGCTGCCTGTATG-CAGGTGTTTCAGGCT
420 430 440 450 460 470 480 490
500 510 520 530 540 550 560
CTGCCCTTTGTACAGGCTCTTTGTTTGTATTTAGGAGAGAAACTGCACCACTCAGGCACTTTTCA
CAAAAATATGATGTGGCTCCGAGGGTGAAGATGAGAAAGTGTAAAGCGCTCACAAGAAAGCCATCATTTT
570 580 590 600 610 620
570 580 590 600 610 620
CAGGGCATACCTGGGCAAGATTACCTTTCTGGCAAGGCATGCCAAGTAGTGTATCC-----TCCT
AGCG-----CTTAAGCAAGAATGCTGTAAAGAAAGAGCGGTGCACGCTTGGCGCAATTCCTGCAGAAAGA
630 640 650 660 670 680 690 700
CTTCACTCTGACTCTCATTCNAATCGGCTCCAAAAAGAGGGATGAGCAGGAGTCTAGAGACTCTGGG
TTGAGAGAAAGAGTCCATTTTGAAGCAGACATGCTGAAGTGTGTCGCGAGAGAGTACAAAGCCCTTATCC
630 640 650 660 670 680 690 700

720 ACC-----CTGGGGAGAGATCTTGGGAGGACCTGGGGAGGNACTCTCAGGAGACTCTGGGGAGAGAGTGG
780

300 310 320 330 340 350 360 370

> O <
O||O IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-085-108-21.res made by tport on Mon 23 Feb 104 9:25:08-PST.

Query sequence being compared: US-10-085-108-21 (1-1041)
Number of sequences searched: 69
Number of scores above cutoff: 69

Results of the initial comparison of US-10-085-108-21 (1-1041) with:

File : 6027924.seq
File : 6475783.seq
File : 6680191.seq
File : US09501104B.seq

100-

N -

U -

50*

N -

B -

E -

R -

O -

F -

10-

S -

E -

Q -

U -

E -

N -

C -

E -

S -

SCORE 0

STDEV 0

116

0

231

347

1

463

2

578

694

3

810

925

1041

4

1041

4

PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 5.00 Window size 500
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 149 Median 10 Standard Deviation 228.29
Times: CPU 00:00:00.01 Total Elapsed 00:00:00.00

Number of residues: 61607
Number of sequences searched: 69
Number of scores above cutoff: 69

The scores below are sorted by initial score.
Significance is calculated based on initial score.

2 100% identical sequences to the query sequence were found:

Sequence Name	Description	Length	Score	Init. Opt.
1. US-09-468-433C-2	Sequence 21, Application	1041	1041	3.91
2. US-09-501-104B-2	Sequence 21, Application	1041	1041	3.91

The list of other best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
3. US-09-066-281B-1	Sequence 18, Application	1983	434	704
4. US-09-468-433C-1	Sequence 18, Application	1983	434	704
5. US-09-501-104B-1	Sequence 18, Application	1983	434	704
6. US-09-066-281B-2	Sequence 20, Application	2940	434	704
7. US-09-468-433C-2	Sequence 20, Application	2940	434	704
8. US-09-501-104B-2	Sequence 20, Application	2940	434	704
9. US-08-845-528C-8	Sequence 8, Application	1691	396	561
10. US-09-066-281B-8	Sequence 8, Application	1691	396	561
11. US-09-468-433C-8	Sequence 8, Application	1691	396	561
12. US-09-501-104B-8	Sequence 8, Application	1691	396	561
13. US-09-468-433C-2	Sequence 25, Application	1224	387	511
14. US-09-501-104B-2	Sequence 25, Application	1224	387	511
15. US-09-468-433C-2	Sequence 23, Application	828	325	399

1. US-10-085-108-21 (1-1041)
US-09-468-433C-2 Sequence 21, Application US/09468433C

Initial Score = 1041 Optimized Score = 1041 Significance = 3.91
Residue Identity = 100% Matches = 1041 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
ATGCTCTCTTTCCAAACCTTCACGCTCAGCTTTCAGGAAGACTTCCAGAACCCGAGTGTGACAGAGAC
|||||
ATGCTCTCTTTCCAAACCTTCACGCTCAGCTTTCAGGAAGACTTCCAGAACCCGAGTGTGACAGAGAC
X      10      20      30      40      50      60      70

      80      90      100      110      120      130      140
TTGTTAGTGCACAGGATTCATAGATGAGGAGGAGGATGCTCTCTCCACCTTCTCTTCTCTCTCTCCAC
|||||
TTGTTAGTGCACAGGATTCATAGATGAGGAGGAGGATGCTCTCTCCACCTTCTCTTCTCTCTCTCTCCAC
      80      90      100      110      120      130      140

      150      160      170      180      190      200      210
TTTTTATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
|||||
TTTTTATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
      150      160      170      180      190      200      210

      220      230      240      250      260      270      280
CTGGGTTCCTCCAGAGATGAGGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
|||||
CTGGGTTCCTCCAGAGATGAGGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
      220      230      240      250      260      270      280

      290      300      310      320      330      340      350      360
CTTCCCGAGGTCCTCCCAAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
|||||
CTTCCCGAGGTCCTCCCAAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
      290      300      310      320      330      340      350      360

      370      380      390      400      410      420      430
TGCTCATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
|||||
TGCTCATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
      370      380      390      400      410      420      430

      440      450      460      470      480      490      500
CATGCCCTTGCCAGAAAGTGAATCCTTGCCCGAGGTATGCCCTGGATGAAAGGTGGCTGAGTTGGTGGCAGTTT

```



```
820 830 840 850 860 870 880
GGGAAGTGTGAGTGCATAGGGGTGTGCTGGAGGAGGACACTTATATATGATGGGATCCAGAAAGCTCC
|||
GGGAAGTGTGAGTGCATAGGGGTATATGCTGGAGGAGGACACTTCTCTATGGGAGCTTGGAGCTCC
1080 1090 1100 1110 1120 1130 1140
TCACATATACATGGGTGCAGAAAGTACCTGGAGTACCGGGAGTGCCCAACAGTGTCTCCCAAGTTATG
|||
TCACATAAAGTTGGGTGCAGAGGACATTTACCTGGAGTATCGGGAGGTGCCCCACAGTTCTCTCCCATATATG
1150 1160 1170 1180 1190 1200 1210 1220
960 970 980 990 1000 1010 1020
AATTTTGTGGGTCCAGAGCCCATTCAGAGGCCAGCAAGA--GAAGTCTTAGAGTTTATCCAGCTAT
|||
AATTCCTGTGGGTCCAGAGCCCATTCAGAAAGCATCAGAAAGAAAGTACTAGAGTTTATAGCAAGCTGA
1230 1240 1250 1260 1270 1280 1290
1030 X
CCAGTATCATCCCTAG
|||
ACAAACATGTTCTAGTTCCTTTCCATCCTGGTACAAGGATGCTTTGAAAGATGTGGAAGAGAGAG
1300 1310 1320 1330 1340 1350
```

6. US-10-085-108-21 (1-1041)

US-09-066-281B-2 Sequence 20, Application US/09066281B

Initial Score = 434 Optimized Score = 704 Significance = 1.25
Residue Identity = 73% Matches = 764 Mismatches = 211
Gaps = 71 Conservative Substitutions = 0

```
1240 1250 1260 1270 1280 1290 1300
CATCCATATCCCTGTGTGATAGCTTTACCTGTCTCTGTAAGAGTGTGCTCCCGTTCCAGGGCTTC
|||
30 40 50 60 70 80 90
CACCCCTCAGTTTGGAGAAAGACTTCCAGAACCCGAGTGTGACAGAGGACTTGGTAGATGCACAGGATCCA
|||
CATTCGCGCAAGTTTGACAAAGACTCCCGGACCTCAGTTGAGTTAGAGACTGGGTAGATGCACAGCATCCA
1310 1320 1330 1340 1350 1360 1370 1380
100 110 120 130 140 150 160
TAGATGAGGAGGAGGAGTCCCTCCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
|||
CAGATGAGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
1390 1400 1410 1420 1430 1440
170 180 190 200 210 220 230
CCTTGTCTCATCTCACCCTTGTCTCACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACC
|||
TCT-----CCACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
1450 1460 1470 1480 1490
```

```
240 250 260 270 280 290 300 310
ATATGCTGCTGTGGGATGCACCTCTTCCCGAGTCTCTAGACTCTCTAGACTCTCTCTCTCTCTCTCTCT
|||
AGGTGCCCTCTGTGTGATACCAATCTTACCGAGA-----GCATTCCCAAGTA
1500 1510 1520 1530 1540
320 330 340 350 360 370 380
TCTTCCCGAGGCTCCCGAGAGTCTCCCGAGGCTCTCTAGACTCTCTAGACTCTCTCTCTCTCTCTCTCT
|||
GTCCTCCACAGGGTCTCCACAGGCTCTCTCCAGAGTCTCTAGACTCTCTCTCTCTCTCTCTCTCTCTCT
1550 1560 1570 1580 1590 1600 1610 1620
```

```
390 400 410 420 430 440 450
CCCAGTGGATGAGGATGCCAGAG---TGAAGAGGAGGATACAGCTACTTTGGCATGCTTTGCCAGAAAGT
|||
GCTCATTCAGTGGAGTCCAGAGCAGCAGAAAGGAGGATACAGGACCTGTGAGGCTCTGAGGCTCTGAGG
1620 1630 1640 1650 1660 1670 1680
```

```
460 470 480 490 500 510 520
AATCCTTGGCCAGCTATGCCCTGATGAAAGTGGCTGAGTTGGTGCAGTTCTTCTCCTCAATATCAAA
|||
AGTCTCTTTACATATACACTAGATGAARAGTGGCCGAGTTAGTGGAGTTCTGCTCTCAATACGAAG
1690 1700 1710 1720 1730 1740 1750
530 540 550 560 570 580 590
CAAAAGAGCCTGTCCAAAGAGCAGAGATGCTGAGCATGTCTATCAAGAAGTATAGGACTATTTTCCCATGA
|||
CAGAGGAGCCTGTAAACAGGAGCAGAGATGCTGATGATTTGTCATC---AGTACAAAGATTTACTTTCTGTGA
1760 1770 1780 1790 1800 1810 1820
```

```
600 610 620 630 640 650 660
TCCTTGGGAAAGCCCATGAGTTCTAGAGCTAATTTTGGCATTTGCCCTGCTGATATGGACCCCGCAACCC
|||
TACTCAAGAGAGCCCGTGGTTTCTAGGAGCTTCTTTTGGCTTGGCTGCTGATAGAGTGGGCCCTTG---ACC
1830 1840 1850 1860 1870 1880 1890
```

```
670 680 690 700 710 720 730
ACTCCTATTTTGAAGACACATTTAGACCTCACCTATGAGGGAAGCTGATTTGATGACCAAGGGCATGCCCA
|||
ACTTCTGTGTGTTGCAACACACAGTACGCTCACCGATGAGGGTAG-----TGAATGATAGGCGCATGCCCG
1900 1910 1920 1930 1940 1950 1960
```

```
740 750 760 770 780 790 800 810
AGAACTGTCTCCTGATTTCTTATCTCAGTATGATCTTTCATAAAGGCGAGCTGTGTCCCGAGGAGGTCTCT
|||
AGAACACCTCTCCTGATTTATTTCTGAGTGTGATCTTTCATAAAGGCAACTGTGCTCTGAGGAGGTCTCTCT
1970 1980 1990 2000 2010 2020 2030
```

```
820 830 840 850 860 870 880
GGGAAGTGTGAGTGCATAGGGGTGTGCTGGAGGAGGACACTTTATATATGCGGATCCCAAGAGCTCC
|||
GGGAAGTGTGCTGAATGCAAGTAGGGGTATGCTGGAGGAGGACACTTCTGCTATGCGGAGCCTTAGGAGCTCC
2040 2050 2060 2070 2080 2090 2100 2110
```

```
890 900 910 920 930 940 950
TCATATACATTTGGTGCAGAAAGTACCTGGAGTACCGGAGGTGCCCAACAGTGTCTCTCCAGCTTATG
|||
TCATTAAGTTTGGGTGCAGGACATTTACCTGGAGTATCGGAGGTGCCCAACAGTGTCTCTCTCATATTTATG
2110 2120 2130 2140 2150 2160 2170
```

```
960 970 980 990 1000 1010 1020
AATTTTGTGGGTGCCAAGGCCCATTCAGAGGCCAGCAAGA--GAAGTCTTAGAGTTTATCCAGCTAT
|||
AATTCCTGTGGGTGCCAAGGCCCATTCAGAAAGCATCAAGAAGAAAGTACTAGAGTTTATAGCAAGCTGA-
2180 2190 2200 2210 2220 2230 2240 2250
```

1030 X

CCAGTATCATCCCTAG

ACAACTGTCTCTTCTTCT

2260 2270 2280 2290 2300 2310

7. US-10-085-108-21 (1-1041)

US-09-468-433C-2 Sequence 20, Application US/09468433C

Initial Score = 434 Optimized Score = 704 Significance = 1.25
Residue Identity = 73% Matches = 764 Mismatches = 211
Gaps = 71 Conservative Substitutions = 0

```
X
|||
ATGCTCTCTCTTCCAAACCTTC
|||
CATCCATATCCCTGTGTGATAGCTTTACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
1240 1250 1260 1270 1280 1290 1300
```

```
X
|||
ATGCTCTCTCTTCCAAACCTTC
|||
CACGCCCTCAGCTTTGAGGAAGACTTCCAGAACCCGAGTGTGACAGAGGACTTGGTAGATGCACAGGATCCA
30 40 50 60 70 80 90
CATTCGCAAGTGTGACACGATCCCGGACCTCAGTTGAGTTAGAGACTGGGTAGATGCACAGCATCCA
|||
```

960 970 980 990 1000 1010 1020
 AATTTTTGGGGTCCAAGAGCCCAATTCAGAGCCAGCAAGA--GAACTCTTAGAGTTTTTTATCCAAGCTAT
 AATTCTGTGGGGTCCAAGAGCCCAATTCAGAGCAAGCATCAAGAAGAAAGTACTAGAGTTTTTTTAGCCAAGCTGTA
 2180 2190 2200 2210 2220 2230 2240 2250
 1030 X
 CCAATATATCCCTAG
 ACAACACTGTTCCTAGTTCTTTCCATCCTCGGTACAAGAGTGCCTTTGAAAGATGTGGAAGAGAGAG
 2260 2270 2280 2290 2300 2310
 8. US-10-085-108-21 (1-1041)
 US-09-501-104B-2 Sequence 20, Application US/09501104B
 Initial Score = 434 Optimized Score = 704 Significance = 1.25
 Residue Identity = 73% Matches = 764 Mismatches = 211
 Gaps = 71 Conservative Substitutions = 0
 X 10 20
 ATGCTCTCTTTTCCAAACCTTC
 CATCATATCCCTGTTGATAGCTTTACCTGTCTCTCTGAAAGATCGTCAATGCCTCCCGTTCCAGGCGTTTC
 1240 1250 1260 1270 1280 1290 1300 1310
 CACSCCTCAGCTTTGAGGAAGACTTCCAGAACCCGAGTGTGACAGAGCACTTGGPAGATGCACAGGATCCCA
 CATTCGCAAGCTTGACAAACGACTCCCGACCTCACTGTTGAGTTGAGTTGAAAGACTGGGTAGATGCACAGCATCCCA
 1310 1320 1330 1340 1350 1360 1370 1380
 100 110 120 130 140 150 160
 TAGATGAGGAGGAGGAGTATGCTCTCTCCACTTCCCTTCCCTTTCCACTTTTATTTCCCTCTCTCTCTCTCT
 CAGATGAGGAGGAGGAGGAGGCTCTCC--GCCTCTTCCACTTTGTACTTAGTATTTTCCCTCTCTCTCTCTCT
 1390 1400 1410 1420 1430 1440
 170 180 190 200 210 220 230
 CTTTGTCTCATCTCACCTTGTCTCTCACCTTACCTCTACTCTCATTTCTGGGTGTTCAGAGAAGATGAGG
 TCT-----CCACATCTCTCTCTGATTTCTTGTGTGTCTCTGAGGAGGAGG
 1450 1460 1470 1480 1490
 240 250 260 270 280 290 300 310
 ATATGCTCTGTCTGGAGTCCACCTCTTCCGAGAGTCTCTCAGATTCCTCCGAGGTCTCTCCCAAGA
 AGGTGCCCTCTCTGTGTGATACCAAACTTTACCGAGA-----GCATTTCCAGTA
 1500 1510 1520 1530 1540 1550
 320 330 340 350 360 370 380
 TCTCTCCGAGGTCCTCCGAGAGTCTTCCGAGAGTCTCTAGACTCTCTAGACTCTCTCATCCCTCTTTGTGA
 GTCCTCCACAGGTCCTCCACAGGTCCTTCCGAGAGTCTCTGAGCTCTCTGCTCTCTCTTTTTCATGGA
 1550 1560 1570 1580 1590 1600 1610 1620
 390 400 410 420 430 440 450
 CCGATTGGATGAGGAGTCCAGAG--TGAAGAGAGGATACACTTGGCATGCTTGGCAGTCTTCCGAGAAAGTG
 GCTCATTTCAAGTGAAGGATCCAGCAGCAGCAAGAGGAGGATACAGCACCTTGTCAAGGCGCTCCAGACAGTGG
 1620 1630 1640 1650 1660 1670 1680
 460 470 480 490 500 510 520
 AATCTTGGCCAGGTATGCCCTGGATGAAAGAGTGCTGAGTGTGAGTTTCTTCTCTCAAAATATCAAAA
 AGTCTCTTTTACATATACACTAGATGAAAGGTGCCGAGTTAGTGGAGTTCTGCTCTCTCAAAATACGAAG
 1690 1700 1710 1720 1730 1740 1750
 530 540 550 560 570 580 590
 CAAAGAGCCTGTGCACAAAGGACGAGATCTCACGACTGTCTATCAAGAAGTATAGGACTATTTTCCCATGA
 CAGAGGAGCCTGTAA CAGAGGACGAGATCTGATGTTGTCATC---AAGTACAAAGATTACTTTCTCTGTGA

```

1760      1770      1780      1790      1800      1810      1820
600      610      620      630      640      650      660
TCTTCGGAAAGCCCATGAGTTTCATAGAGCTAAATTTTGGCAATTGCCCTGACTGATATGACCCCGCAACAC
TACTCAAGAGAGCCCGTGAAGTTCATGGAGCTCTCTTTTGGCTTGCCTGATAGAGTGGGCCCTG---ACC
1830      1840      1850      1860      1870      1880      1890
670      680      690      700      710      720      730
ACTCCTATTTCTTTGAACACACATAGACCTCACTCATGAGGGAAGCCTGATTGATGACCAAGGCGCATGCCCA
ACTTCTGTGTGTTTGCAACACACAGTAGGCCCTCACCGATGAGGTAG-----TGATGATGAGGCGCATGCCCG
1900      1910      1920      1930      1940      1950      1960
740      750      760      770      780      790      800      810
AGAACTGTCTCTGATTTCTTATTTCTCAGATATGATCTTCATAAAGGCGAGCTGTCTCCCGAGGAGTTCATCT
AGAACAGCTCCTCATTAATTATTTCTGAGTGTGATCTTCATPAAGGGCAATGTGTCCCTCTGAGAGGTCACTC
1970      1980      1990      2000      2010      2020      2030
820      830      840      850      860      870      880
GGGAAGTGTGAGTGCAAATAGGGGTGTGTCTGGGAGGGAGCACTTTATATATGGGATCCCAAGAAAGTCTGC
GGGAAGTGTCTGAATGCAGTAGGGGTATATGCTGGAGGGAGCACTTCGTCTATGGGAGCGCTTAGGAGTCTC
2040      2050      2060      2070      2080      2090      2100
890      900      910      920      930      940      950
TCACTATACATTTGGGTGCAGAGAAAGTACCTTGGAGTACCGGAGTGCCTCCAAAGTGTCTCTCCACGTTATG
TCACTAAAGTTTGGTGCAGGCAATTACTTGGAGTATCGGAGGTGCCCAAGTTCCTCCCATTAATTATG
2110      2120      2130      2140      2150      2160      2170
960      970      980      990      1000      1010      1020
AATTTTGTGGGTGCCAAGAGCCCATTCAGAGGCGCACAAGA--GAACTCTTAGAGTTTTTATTCCAAGCTAT
AATTCCTGTGGGTCCAAGAGCCCATTCAGAAAGCATCAGAGAGAAAGTACTAGATTTTATGCCAAGCTGA
2180      2190      2200      2210      2220      2230      2240      2250
1030      X
CCAGTATCATCCCTAG
ACAACATGTTCTTAGTTCCCTTCCATCTCTGTTACAGGATGCTTTGAAGAGATGTGGAAGAGAGAG
2260      2270      2280      2290      2300      2310
US-10-085-108-21 (1-1041)
US-08-845-528C-8 Sequence 8, Application US/08845528C

Initial Score      = 396      Optimized Score      = 561      Significance      = 1.08
Residue Identity  = 57%      Matches          = 612      Mismatches      = 415
Gaps              = 44      Conservative Substitutions

X      10      20      30      40
ATGCCTCTCTTTCCAAACCTTCCAGCCTCAGCTTTGAGG--AAGACTTCC
10      20      30      40      50      60      70
CCATCTGAGGGACGGGTAGAGTTTCGGCCGAAGAACCTTGACCCAGGCTCTGTGAGGAGGCAAGGTTTTC
100      110      120      130      140
50      60      70      80      90      100      110
AGAACCGAGTGTGACAGAGGACTTGTAGATGCACAGGATTCATAGATGAGGAGGAGAGA-----TGC
GGGACACAGGCCAACCCAGAGGAC-----AGAGATCCCTGGAGGGCCACAGAGGACCAAGAGGAGAAGATCTGC
80      90      100      110      120      130      140
120      130      140      150      160      170      180      190      200      210
CTCCTCCACATTCCTTCCCTTTCACACTTTTATTCCTCCCTCTCTCTCTTCTTCTGCTCATCTCCACCTT
CTGTGGGTCTTTCATTGCCAGCTCCTGCCACACATCTCGTGCCTGCTGCTGCTGACGAGAGTCAATGTCCTCTT
150      160      170      180      190      200      210
190      200      210      220      230      240      250
GTCTCTCACCTTACCTCTACTCTCATCTTCTGGGTGTTCCAGAGATGAGGATATGCTCTGCTGGG---AT

```

[illegible]

CTATTTCTTTTGAGACACATTAGACCTCACTATGAGGAAGCCTGATTGATGACCGGCGATGCCCAAGA

GCAGAGTCCTCCGCCAGAGTCCTAGACTCTGCTC-----ATCCCTCTTTTGTGGAC

GAGTCCAGCAGTGAAGAGGAGGATACAGCTA----CTTGGCATGCTTCCGAGAAAGTGAATCTTGGCCGAGG
 470 480 490 500 510 520 530 540 550 560 570
 GCTCCGAGGGTGAAGATGAGGAAAGTGAAGCGCTCACAGAAAGCCATCATTTTAAAGCGGCTTAAGCAAA
 510 520 530 540 550 560 570
 TATGCCCTGGATGAAGAGTGGCTGAGTTGTCAGTTTCTTCCCTCAATATCAACAAAAGAGCGCTGTC
 580 590 600 610 620 630 640
 GATGCTGTAAAGAAAGAGGGCGTGACGCTTGCGGCAATTCTCGAAGAAGAGTTTGAGAAGAAGAGTCCATT
 540 550 560 570 580 590 600
 ACAAAAGCAGAGATGCTGACGACTGTCAACAAGATATAAGGACTATTTTCCCATGATCTTCGGGAAAGCC
 610 620 630 640 650 660 670 680
 TTGAAGGCAGACATGCTGAAGTGTGTCGAGAGAGTACAAAGCCCTACTTCCCTCAGATCCTCAACAGAACG
 650 660 670 680 690 700 710 720
 CATGAGTTCATAGAGCTAAATTTTGGCATTTGCCCTGATGATGAGCCCGCAACCACTCCTCTATTTCTTT
 610 620 630 640 650 660 670 680
 TCCCAACATTTGGTGTGGCTTTGGCTTTGAATTGAATGAAGAAATGAATTCACGCGGCGAGTCTCTACACCTT

GAAGACATTTAGACCTCACCTATGAGGGAGGCTGATTGATGACCAGGCGATGCCCAAACTGTCTCTG
GTCAGCAGCTAGGCGCTCCCGATGAGGAATTTCTGAGTGGTGATATGGCGCTGCCGAAGTCGGGHTCTCTG

ATTCTTATTCACAGTATGATCTTCAATAAAGCGACGTGTCCCGAGGAGGTCATCTCGGAAGTGTGATG
ATGTCGCTCCTGGTTGTGATCTTTCATGAACGGCAACTGTCCCACTGAAGAGGAGGTCTGGAGTCTCTGGGT
GCAATAGGGGTGTCTGTGGGAGGAGCACTTATATATATGGGATCCAGAAAGTCTCTCACTATACATTTGG
CTGTTGGGGATATATATGATGGATCCTTCAATCTATGGGATGCTCGGAAGATCATTTACTTGAAGATTTG

[illegible]

```

1. US-10-085-108-21 (1-1041)
US-09-501-104B-2 Sequence 25, Application US/09501104B

Initial Score = 387 Optimized Score = 511 Significance = 1.04
Missive Identity = 50% Matches = 580 Mismatches = 461
Gaps = 113 Conservative Substitutions = 0

X      10      20      30      40      50      60      70
ATGCCTCTCTTCCAAACCTTCCAGCGCTCAGCTTTTCAGAGAGACTTCCAGAACCCGAGTGTGCACAGAGAC
|||||
ATGCCTGGGGTTCACAGAGTAAGCTCCGTACCTGTGAGAAACGCCAAGAGAGACCAATGGTGCACCCACAGGT
10      20      30      40      50      60      70
X

```

```
Initial Score      = 387  Optimized Score = 511  Significance = 1.04
Residue Identity  = 50%  Matches      = 580  Mismatches = 461
Gaps              = 113  Conservative Substitutions = 0
```

X 1.0 2.0 3.0 4.0 5.0 6.0 7.0
 ATGCGCTCTCTTTCCAAACCTTCCACGCTCTAGCTTTGAGGAGACTTCCAAACCCAGTGTGACAGAGAC
 ||||| || || || || || || || || ||
 ATGCGCTCGGGGTACAAAGAGTAAAGTCCGTACTGTGAGAAACGCCAAGACCAATGCTTGCCACAGGGT
 X 1.0 2.0 3.0 4.0 5.0 6.0 7.0

GCATAGGGGTGTGTCTGGGAGGAGCACTTTATATATGGGATCCAGAAAGCTGCTCACTATACATGGG
CTGTTGGGATATATGATGGATCTCTGCATTCATCTATGGGATGCTCGCAAGATCATTAATCGAATTTG
940 950 960 970 980 990 1000 1080

900 910 920 930 940 950 960
GTGCAGAGAAAGTACCTGGAGTACCGGAGGTGCCAAAGTGTCTCTCCACGTTATGAATTTTGTGGGT
GTGCAAGATAGTACGTGGTTTACCGGAGGTGTGCAACAGATGATCTCTCCATGCTATGAGTTCCTGTGGGT
1010 1020 1030 1040 1050 1060 1070 1080

970 980 990 1000 1010 1020 1030
CCAAGAGCCCATTCAGAGGCCAGCAAGA--GAAGTCTTAGAGTTTATCCAAGCTATCAGTATCATCCCT
CCAGAGCCTATGCTGAACCCACCAAGATGAGAGTCTGGTGTGTTTGGCCGACAGCAACACCAAGTCCC
1090 1100 1110 1120 1130 1140 1150

1040
AG
|
GGTTTATACCCACATCTGTATGAAGAGCGCTTTGATAGATGAGGTAGAGAGAG
X 1160 1170 1180 1190 1200

15. US-10-085-108-21 (1-1041)
US-09-468-433C-2 Sequence 23, Application US/09468433C

Initial Score = 325 Optimized Score = 399 Significance = 0.77
Residue Identity = 59% Matches = 409 Mismatches = 278
Gaps = 4 Conservative Substitutions = 0

310 320 330 340 350 360 370
TCCCAAGATCTCTCCCGAGGCTCTCCGAGAGCTCTCCCGAGAGTCTTAGACTCCCTGCTCATCCCTCT
ATGACCTCTCGAGGTGTTTATA
X 10 20

380 390 400 410 420 430 440
TTTGTGACCCGATTCGATGAGAGTCCAGAGTGAAGGAGGTACAGTACTTGGCATGCTTCCGCA
ATGCAGAGTCTGA--CGAAAGGGCTAACCATAGATAGATAGAGTCCCATGTTCTCCAGAGGCTCTCACCTTC
30 40 50 60 70 80 90

450 460 470 480 490 500 510
AAGTGAATCTTTGCCAGGTATGCCCTGGATGAAGGTGGCTGAGTTGGTGAGTTCTTCTCTCAATA
CACTGAGATTATGACGCAATTTCAATAATTAAGGTGGGTCTTTGGAGCAGTCTCTGCTCTACAAGT
100 110 120 130 140 150 160

520 530 540 550 560 570 580 590
TCAACAAAGAGCCTGTCAAAAGCAGAGATGCTGACGACTGTATCAAGAGTATAGGACTATTTCC
CAAAATGAACACGCGTATTTGAGGAAGATGATCTGGAAGTTGTCAACCCCAAGATACCAAAACCAAGTTTGC
170 180 190 200 210 220 230

600 610 620 630 640 650 660
CATGATCTTTGGGAGGCCCATGATTCATAGAGTAAATTTTGGCATTTGCCCTGACTGATATGGACCCGA
TGAGATTCAAGAAGAGCTTCGAGCACAATTGAGGTGTCTTTGAGTTGACTTGAAGGAGTCAACCCCAAC
240 250 260 270 280 290 300

670 680 690 700 710 720 730
CAACACTCTATTCTTTGAAGACACATTAGACTCACCTATGAGGAGGCTGATTCATGACACAGGCGAT
TTGTCACTTATATGACCTTGTGAGCAAGCTGAAACTCCCAAAATGGGAGGATTCATGTGGCAAGTGT
310 320 330 340 350 360 370 380

740 750 760 770 780 790 800
GCCAGAGACTGCTCTCTGATTTCTTATTTCTCAGTATGATCTTCATAAAGGCGAGCTGTGTCCCGAGGAGGT
ACCCAGACTGGTCTCTCATGACTTTCCTGTTGTGATCTTCTGAAAGGCAACTGTGCCCAACAGGAGA
390 400 410 420 430 440 450

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 01:49:48 ; Search time 197 Seconds
(without alignments)
392.672 Million cell updates

Title: US-10-085-108-21 COPY 711 731

Perfect score: 21
Sequence: 1 AAGCCTGATTGATGACCAGGG 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 490076

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Minimum DB seq length: 0
Maximum DB seq length: 21
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
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16: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

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SUMMARIES

Result No.	Score	Query *		DB	ID	Description
		Match	Length			
C	1	12.8	61.0	20	12	US-10-189-266-49
	2	12.8	61.0	20	12	US-10-189-266-118
	3	12.6	60.0	21	13	US-10-115-223-33
	4	12.4	59.0	20	13	US-10-251-593-93
	5	12.2	58.1	17	9	US-08-866-108-8495
C	6	12.2	58.1	17	9	US-08-866-108-8495
	7	12	57.1	20	13	US-10-168-989-15
	8	12	57.1	21	15	US-10-090-011-60
	9	11.8	56.2	20	12	US-10-189-266-48
	10	11.8	56.2	20	12	US-10-189-266-117
C	11	11.6	55.2	18	13	US-10-219-195-47
	12	11.6	55.2	20	10	US-09-508-500A-4
	13	11.6	55.2	20	12	US-10-159-856-41
	14	11.6	55.2	20	11	US-10-159-856-106
	15	11.6	55.2	21	11	US-09-382-860-144
	16	11.6	55.2	21	11	US-09-382-860-144
	17	11.6	55.2	21	11	US-09-382-860-144
	18	11.6	55.2	21	11	US-09-382-860-144
	19	11.6	55.2	21	11	US-09-382-860-144
	20	11.6	55.2	21	11	US-09-382-860-144

16	11.6	55.2	21	13	US-10-278-437-22	Sequence 22, Appl
17	11.6	55.2	21	15	US-10-001-670-35	Sequence 35, Appl
18	11.6	55.2	21	15	US-10-278-455-22	Sequence 22, Appl
C 19	11.4	54.3	15	15	US-10-056-414-31	Sequence 31, Appl
C 20	11.4	54.3	15	15	US-10-056-414-220	Sequence 220, Appl
C 21	11.4	54.3	17	10	US-09-864-785-63	Sequence 63, Appl
C 22	11.4	54.3	17	10	US-09-864-785-1452	Sequence 1452, Ap
C 23	11.4	54.3	17	10	US-09-864-785-2693	Sequence 2693, Ap
C 24	11.2	53.3	17	9	US-09-866-108-7176	Sequence 7176, Ap
C 25	11.2	53.3	17	9	US-09-866-108-7177	Sequence 7177, Ap
C 26	11.2	53.3	17	9	US-09-866-108-8494	Sequence 8494, Ap
C 27	11.2	53.3	17	9	US-09-866-108-8497	Sequence 8497, Ap
C 28	11.2	53.3	18	10	US-09-969-373-1731	Sequence 1731, Ap
C 29	11.2	53.3	19	12	US-10-349-143-4273	Sequence 4273, Ap
C 30	11.2	53.3	19	13	US-10-356-625-111	Sequence 111, Appl
C 31	11.2	53.3	20	11	US-09-739-909-25	Sequence 25, Appl
C 32	11.2	53.3	20	12	US-10-159-856-5	Sequence 5, Appl
C 33	11.2	53.3	20	12	US-10-289-762-6317	Sequence 6317, Ap
C 34	11.2	53.3	20	13	US-10-172-094-105	Sequence 105, Appl
C 35	11.2	53.3	20	13	US-09-964-0598-10	Sequence 10, Appl
C 36	11.2	53.3	20	13	US-10-363-798-24	Sequence 24, Appl
C 37	11.2	53.3	20	13	US-10-168-989-10	Sequence 10, Appl
C 38	11.2	53.3	20	13	US-10-148-355A-89	Sequence 89, Appl
C 39	11.2	53.3	20	13	US-10-438-075-27	Sequence 27, Appl
C 40	11.2	53.3	20	15	US-10-072-094-105	Sequence 105, Appl
C 41	11.2	53.3	20	15	US-10-173-539-21	Sequence 21, Appl
C 42	11.2	53.3	20	15	US-10-152-297-110	Sequence 110, App
C 43	11.2	53.3	21	13	US-10-184-085A-211	Sequence 211, App
C 44	11.2	53.3	21	13	US-10-149-407-7	Sequence 7, Appl
C 45	11	52.4	18	10	US-09-969-373-1577	Sequence 1577, Ap

ALIGNMENTS

```

RESULT 1
US-10-189-266-49/c
; Sequence 49, Application US/10189266
; Publication NO. US20040006029A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELL DIVISION CYCLE 2 EXPRESSION
; FILE REFERENCE: RTS-0384
; CURRENT APPLICATION NUMBER: US/10/189,266
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 150
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-266-49

```

CURRENT APPLICATION NUMBER: US/10/189,266
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 118
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-189-266-118

Query Match 61.0%; Score 12.8; DB 12; Length 20;
Best Local Similarity 87.5%; Pred. No. 6.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TGATTGATGACCAGG 21
|||||
Db 1 TGATTGACAAAGG 16

RESULT 3
US-10-115-223-33
Sequence 33, Application US/10115223
Publication No. US20030176334A1
GENERAL INFORMATION:
APPLICANT: Brooks, Peter
APPLICANT: Chersesh, David A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
FILE REFERENCE: MER00495
CURRENT APPLICATION NUMBER: US/10/115,223
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US/09/194,468
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/018,773
PRIOR FILING DATE: 1996-05-31
PRIOR APPLICATION NUMBER: 60/015,896
PRIOR FILING DATE: 1996-05-31
PRIOR APPLICATION NUMBER: PCT/US97/09158
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotide primer
US-10-115-223-33

Query Match 60.0%; Score 12.6; DB 13; Length 21;
Best Local Similarity 78.9%; Pred. No. 8.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCTGATTGATGACCAGG 21
|||||
Db 1 GCCGGATCCATGACCAAGT 19

RESULT 4
US-10-251-598-93
Sequence 0, Application US/10251598
Publication No. US20030170668A1
GENERAL INFORMATION:
APPLICANT: Detera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berretkinn, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic

Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/251,598
FILING DATE: 19-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952
FILING DATE: 19-Apr-1999
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: D18S1299 reverse primer
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1...20
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-10-251-598-93

Query Match 59.0%; Score 12.4; DB 13; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GATTGATGACCAGG 20
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Db 2 GATTGAGGACCAGG 15

RESULT 5
US-09-866-108-8495
Sequence 8495, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOmica-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8495
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8495

Query Match 58.1%; Score 12.2; DB 9; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCTGATTGATGACCA 18
||||| ||||| |||||
Db 1 AGCTGTTGATGAGCA 17

RESULT 6
US-09-866-108-8495
; Sequence 8496, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8496
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8496

Query Match 58.1%; Score 12.2; DB 9; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCTGATTGATGACCAG 19
||||| ||||| |||||
Db 1 GCCTGTTGATGAGCAG 17

RESULT 7
US-10-168-989-15/c
; Sequence 15, Application US/10168989
; Publication No. US20030190631A1
; GENERAL INFORMATION:
; APPLICANT: Chartier-Harlin et al.
; TITLE OF INVENTION: Implication of a known gene named CP2/LSF-LBP-1 in
; FILE REFERENCE: P07666US00/BAS
; CURRENT APPLICATION NUMBER: US/10/168,989
; CURRENT FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-168-989-15

Query Match 57.1%; Score 12; DB 13; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCTGATTGATGACCAGG 21
||||| ||||| |||||
Db 20 AGCCAGATTTACAGCAGG 1

RESULT 8
US-10-090-011-60/c
; Sequence 60, Application US/10090011
; Publication No. US20030082810A1
; GENERAL INFORMATION:
; APPLICANT: Serup, Palle
; APPLICANT: Heimberg, Harry
; APPLICANT: Gradwohl, Gerard
; TITLE OF INVENTION: Methods For Generating Insulin-Secreting
; Cells Suitable for Transplantation

Qy 2 AGCCTGATTGATGACCAG 19

Db 2 AGCCGAGTGCTGACCAG 19
|||||

RESULT 13

US-10-159-856-41/c
; Sequence 41, Application US/10159856
; Publication No. US20030228689A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRESSION
; FILE REFERENCE: RTS-0365
; CURRENT APPLICATION NUMBER: US/10/159,856
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-856-41

Query Match 55.2%; Score 11.6; DB 12; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.9e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCTGATTGATGACCAGG 21
|||
Db 19 CTTGCTGGATGACCAGG 2

RESULT 14

US-10-159-856-106
; Sequence 106, Application US/10159856
; Publication No. US20030228689A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRESSION
; FILE REFERENCE: RTS-0365
; CURRENT APPLICATION NUMBER: US/10/159,856
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-159-856-106

Query Match 55.2%; Score 11.6; DB 12; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.9e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCTGATTGATGACCAGG 21
|||
Db 2 CTTGCTGGATGACCAGG 19

RESULT 15

US-09-382-860-144
; Sequence 144, Application US/09382860
; Publication No. US20030110526A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Jr., Robert H.
; APPLICANT: Liu, Jing
; APPLICANT: Aoki, Masashi
; APPLICANT: Hoffman, Eric
; APPLICANT: Chou, Fan-li
; TITLE OF INVENTION: DYSFERLIN MUTATIONS
; FILE REFERENCE: 00786/401002

; CURRENT APPLICATION NUMBER: US/09/382,860
; CURRENT FILING DATE: 1999-08-25
; EARLIER APPLICATION NUMBER: US 60/097,930
; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-382-860-144

Query Match 55.2%; Score 11.6; DB 11; Length 21;
Best Local Similarity 77.8%; Pred. No. 2.9e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCTGATTGATGACCAGG 20
|||
Db 4 GCCTGAGGATCAGCAGG 21

Search completed: February 20, 2004, 04:09:31
Job time : 198 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 00:42:09 ; Search time 45.5 seconds
(without alignments)
203.715 Million cell updates/sec

Title: US-10-085-108-21_COPY_711_731

Perfect score: 21
Sequence: 1 AAGCTGATGATGACAGGG 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 352324

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgm2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgm2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgm2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgm2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.8	61.0	19	US-08-200-232-16	Sequence 16, Appl
2	12.8	61.0	19	PCT-US95-02219-16	Sequence 16, Appl
3	12.8	61.0	19	PCT-US95-02219A-17	Sequence 17, Appl
4	12.6	60.0	21	US-09-194-468A-33	Sequence 33, Appl
5	12.4	59.0	15	US-08-363-240A-560	Sequence 560, Appl
6	12.4	59.0	19	US-09-050-159-38	Sequence 38, Appl
7	12.4	59.0	20	US-09-091-952A-93	Sequence 93, Appl
8	12.2	58.1	20	US-09-658-679A-61	Sequence 61, Appl
9	11.8	56.2	21	US-08-171-718-7	Sequence 7, Appl
10	11.8	56.2	21	US-08-478-087-7	Sequence 7, Appl
11	11.8	56.2	21	US-09-081-149-17	Sequence 17, Appl
12	11.6	55.2	19	US-08-363-233B-7	Sequence 7, Appl
13	11.6	55.2	20	US-08-809-297-30	Sequence 30, Appl
14	11.6	55.2	20	US-09-554-511-20	Sequence 20, Appl
15	11.6	55.2	21	US-08-874-825-35	Sequence 35, Appl
16	11.6	55.2	21	US-08-954-536-7	Sequence 7, Appl
17	11.6	55.2	21	US-08-954-536-7	Sequence 7, Appl
18	11.6	55.2	21	US-09-387-699-22	Sequence 22, Appl
19	11.6	55.2	21	US-09-231-303-35	Sequence 35, Appl
20	11.6	55.2	21	US-09-641-259B-22	Sequence 22, Appl
21	11.4	54.3	15	US-08-291-932A-31	Sequence 31, Appl
22	11.4	54.3	15	US-08-291-932A-31	Sequence 22, Appl
23	11.4	54.3	15	US-08-363-240A-561	Sequence 561, Appl
24	11.4	54.3	15	US-08-363-240A-561	Sequence 561, Appl
25	11.4	54.3	20	US-09-954-550-37	Sequence 37, Appl
26	11.2	53.3	18	US-08-284-485-11	Sequence 11, Appl
27	11.2	53.3	18	US-09-580-189-12	Sequence 12, Appl

28	11.2	53.3	19	US-09-422-978-4273	Sequence 4273, Appl
29	11.2	53.3	19	US-09-230-652-111	Sequence 111, Appl
30	11.2	53.3	20	US-08-044-618-2	Sequence 2, Appl
31	11.2	53.3	20	US-08-334-545-8	Sequence 8, Appl
32	11.2	53.3	20	US-08-827-036A-13	Sequence 13, Appl
33	11.2	53.3	20	US-09-147-933-48	Sequence 48, Appl
34	11.2	53.3	20	US-09-467-642-89	Sequence 89, Appl
35	11.2	53.3	20	US-09-383-316-110	Sequence 110, Appl
36	11.2	53.3	20	US-09-792-594-14	Sequence 14, Appl
37	11.2	53.3	20	US-09-198-452A-6317	Sequence 6317, Appl
38	11.2	53.3	21	US-08-555-723B-8	Sequence 8, Appl
39	11.2	53.3	21	US-09-123-465-8	Sequence 8, Appl
40	11	52.4	19	US-07-977-284A-21	Sequence 21, Appl
41	11	52.4	19	US-08-256-426B-21	Sequence 21, Appl
42	11	52.4	20	US-09-596-938-9	Sequence 9, Appl
43	11	52.4	21	US-08-690-734A-44	Sequence 44, Appl
44	11	52.4	21	US-08-742-185-44	Sequence 44, Appl
45	11	52.4	21	US-09-305-927-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-200-232-16
; Sequence 16, Application US/08200232
; Patent No. 5721349
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND RELATED METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,232
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-200-232-16

Query Match 61.0%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGCTGATGATGATGAC 16

Db 1 AAGCTGATGATGATGAC 16

RESULT 2
PCT-US95-02219-16
; Sequence 16, Application PC/TUS9502219
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND RELATED METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02219
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-9880
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-02219-16
Query Match 61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGCTTGATTGATGAC 16
Db 1 AAGCTTGATTGATGAC 16
RESULT 3
PCT-US95-02219A-17
; Sequence 17, Application PC/TUS9502219A
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Tummuru, Murali KR
; APPLICANT: Cao, Ping
; APPLICANT: Thompson, Stuart A.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND THE RELATED METHODS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02219A
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 2200.023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-02219A-17
Query Match 61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGCTTGATTGATGAC 16
Db 1 AAGCTTGATTGATGAC 16
RESULT 4
US-09-194-468A-33
; Sequence 33, Application US/09194468A
; Patent No. 650924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheres, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER00498
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide primer
US-09-194-468A-33
Query Match 60.0%; Score 12.6; DB 4; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 GCCTGATTGATGACCGGG 21
Db 1 GCCGGATCCATGACCAGTG 19
RESULT 5
US-08-363-240A-560/c
; Sequence 560, Application US/08363240A
; Patent No. 5705388

GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR PREVENTION, INHIBITION OF PROGRESSION AND REGRESSION OF VASCULAR DISEASES
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 560:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-560

Query Match 59.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTGATTGATGACCA 18
Db 14 CTGATTGATGACCA 1

RESULT 6
US-09-050-159-38
Sequence 38, Application US/09050159A
Patent No. 6197505
GENERAL INFORMATION:
APPLICANT: No. 6197505berg, Leif T
APPLICANT: Andersson, Maria K
APPLICANT: Linstrom, Per H
TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND TITLE OF INVENTION: COMPOSITIONS FOR USE THEREOF
FILE REFERENCE: 1248/1D042
CURRENT APPLICATION NUMBER: US/09/050,159A
CURRENT FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/042,930
EARLIER FILING DATE: 1987-04-03
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38

LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-09-050-159-38

Query Match 59.0%; Score 12.4; DB 3; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGCCTGATTGATGA 15
Db 4 AGCCTGATTGATGA 17

RESULT 7
US-09-091-952A-93
Sequence 93, Application US/09091952A
Patent No. 6458532
GENERAL INFORMATION:
APPLICANT: Detera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1...20
OTHER INFORMATION: D18S1299 reverse primer
SEQUENCE DESCRIPTION: SEQ ID NO: 93:

US-09-091-952A-93

Query Match 59.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.5e-03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GATTGATGACGAGG 20
||||| |||||
Db 2 GATTGAGGACGAGG 15

RESULT 8

US-09-658-679A-61/C
; Sequence 61, Application US/09658679A
; Patent No. 644464
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; TITLE OF INVENTION: Antisense Modulation of E2F Transcription Factor 2 Expression
; FILE REFERENCE: R15-0186
; CURRENT APPLICATION NUMBER: US/09/658,679A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-679A-61

Query Match 58.1%; Score 12.2; DB 4; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.9e-03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCTGATTGATGACGAGG 20
||||| ||||| |||||
Db 18 CCTGACTGAGGACGAGG 2

RESULT 9

US-08-171-718-7
; Sequence 7, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; INFORMATION FOR SEQ ID NO: 7:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-171-718-7

Query Match 56.2%; Score 11.8; DB 1; Length 21;
Best Local Similarity 86.7%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCTGATTGATGAC 16
||||| ||||| |||||
Db 5 AACCTGATTGATGAC 19

RESULT 10

US-08-478-087-7
; Sequence 7, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,087
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,718
; FILING DATE: 22-DEC-1993
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:

; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
US-08-809-297-30

Query Match 55.2%; Score 11.6; DB 2; Length 20;
Best Local Similarity 77.8%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGCTGATTGATGACCAG 19
Db 18 AGCATGATCATGACCTG 1

RESULT 14
US-09-554-511-20
; Sequence 20, Application US/09554511
; Patent No. 6312928
; GENERAL INFORMATION:
; APPLICANT: VAN GEMEN, Bob
; APPLICANT: VAN STRIUP, Dianne A.M.
; APPLICANT: SCHUKKINK, Adriana F.
; TITLE OF INVENTION: TRANSCRIPTION BASED AMPLIFICATION OF DOUBLE STRANDED
; FILE REFERENCE: VAN GEMEN ET AL.
; CURRENT APPLICATION NUMBER: US/09/554,511
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: PCT/EP98/07329
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: EP 97203577.8
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: HUMAN
US-09-554-511-20

Query Match 55.2%; Score 11.6; DB 4; Length 20;
Best Local Similarity 77.8%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCCTGATTGATGACCAG 20
Db 1 GCTTGATGATGACCATG 18

RESULT 15
US-08-874-825-35
; Sequence 35, Application US/08874825
; Patent No. 6057101
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Yang, Meijia
; APPLICANT: Knight, James
; APPLICANT: Kalbfleisch, Theodore
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
; TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York

; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,825
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,824
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-874-825-35

Query Match 55.2%; Score 11.6; DB 3; Length 21;
Best Local Similarity 66.7%; Pred. No. 4e+03;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCTGATTGATGACCGGG 21
Db 2 CCUGAUGGAGACCGGG 19

Search completed: February 20, 2004, 02:40:59
Job time : 46.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 00:32:29 ; Search time 1490 Seconds
(without alignments)
342.546 Million cell updates/sec

Title: US-10-085-108-21_COPY_711_731

Perfect score: 21

Sequence: 1 AAGCTGATTGATGACGAGG 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 8380

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estim.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10.2	48.6	20	28	AZ600911 IM0418M21
C 2	10.2	48.6	21	28	AZ306912 IM008L07
C 3	9.8	46.7	19	28	AZ763729 IM0559N16
C 4	9.8	46.7	21	28	AZ504285 IM0344J20

C 5	9.4	44.8	19	14	C01992	C01992 HUMGS000401
C 6	9.4	44.8	21	28	AZ771145	AZ771145 IM0573A09
C 7	9.2	43.8	21	28	AZ509602	AZ509602 IM0352E08
C 8	9.2	43.8	21	28	AZ661528	AZ661528 IM0540I06
C 9	9.2	43.8	21	28	AZ662959	AZ662959 IM0542P18
C 10	9.2	43.8	21	28	AZ774704	AZ774704 2M0004G18
C 11	8.8	41.9	16	12	BM395054	BM395054 50072-2-7
C 12	8.8	41.9	19	14	C01993	C01993 HUMGS000401
C 13	8.8	41.9	21	28	AZ987077	AZ987077 2M0269H04
C 14	8.6	41.0	18	13	BQ594466	BQ594466 E012442-0
C 15	8.6	41.0	20	28	AZ307610	AZ307610 IM0009G15
C 16	8.6	41.0	20	28	AZ462631	AZ462631 IM0269F12
C 17	8.6	41.0	20	28	AZ665083	AZ665083 IM0545O15
C 18	8.6	41.0	21	28	AZ405406	AZ405406 IM0174P08
C 19	8.4	40.0	15	14	CA796369	CA796369 Cac BL_33
C 20	8.4	40.0	19	9	AW249918	AW249918 2821753.3
C 21	8.4	40.0	19	28	AZ808212	AZ808212 2M0071D03
C 22	8.4	40.0	20	28	AZ308421	AZ308421 IM0011E19
C 23	8.4	40.0	20	28	AZ473322	AZ473322 IM0289H08
C 24	8.2	39.0	19	28	AZ491924	AZ491924 IM0325G16
C 25	8.2	39.0	19	28	AZ655467	AZ655467 IM0530O17
C 26	8.2	39.0	19	28	AZ655870	AZ655870 IM0531N06
C 27	8.2	39.0	19	28	AZ815827	AZ815827 2M0084X23
C 28	8.2	39.0	19	28	AZ875430	AZ875430 2M0189K09
C 29	8.2	39.0	19	28	AZ937956	AZ937956 2M0196O18
C 30	8.2	39.0	19	28	AZ989459	AZ989459 2M0272M17
C 31	8.2	39.0	19	28	AZ990851	AZ990851 2M0274E15
C 32	8.2	39.0	20	29	TA345E06Q	TA345E06Q T. brucei
C 33	8.2	39.0	21	9	AW332721	AW332721 S12A10 AG
C 34	8.2	39.0	21	28	AZ796024	AZ796024 2M0051N12
C 35	8.2	39.0	21	28	AZ806895	AZ806895 2M0069E13
C 36	8	38.1	19	28	AZ303949	AZ303949 IM0003M19
C 37	8	38.1	19	28	AZ810098	AZ810098 2M0074N21
C 38	8	38.1	19	28	AZ836630	AZ836630 2M0131J05
C 39	8	38.1	19	28	AZ849303	AZ849303 2M0150K08
C 40	8	38.1	20	9	AU254575	AU254575 AU254575
C 41	8	38.1	20	13	BQ583464	BQ583464 E011979-0
C 42	8	38.1	21	28	AZ775019	AZ775019 2M0004L20
C 43	7.8	37.1	19	12	BM396288	BM396288 5009-0-2-
C 44	7.8	37.1	19	28	AZ486389	AZ486389 IM0314E21
C 45	7.8	37.1	19	28	AZ621254	AZ621254 IM0454E20

ALIGNMENTS

RESULT 1
AZ600911/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ600911 20 bp DNA linear GSS 13-DEC-2000
IM0418M21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0418M21 R, genomic survey sequence.
AZ600911.1 GI:11723101
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0418 row: M column: 21
 Seq primer: CACACAGGAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

source

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1. .20
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0418M21"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

BASE COUNT 2 a 7 c 6 g 5 t
 ORIGIN

```
Query Match 48.6%; Score 10.2; DB 28; Length 20;
Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGATTGATGACACAGG 20
    ||||| |||||
Db 18 TGATGCGGACACAGG 4
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RESULT 2
AZ306912
LOCUS
DEFINITION
  1M0008L07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0008L07 F, genomic survey sequence.
ACCESSION
  AZ306912
VERSION
  AZ306912.1 GI:10345389
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 21)
REFERENCE
  1 (bases 1 to 21)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
  ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
  and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
```

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0008 row: L column: 07
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

source

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1. .21
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0008L07"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

BASE COUNT 7 a 2 c 6 g 6 t
 ORIGIN

```
Query Match 48.6%; Score 10.2; DB 28; Length 21;
Best Local Similarity 80.0%; Pred. No. 5.4e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGATTGATGACACAGG 20
    ||||| |||||
Db 1 TGATTATGCGGAGG 15
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RESULT 3
AZ763729
LOCUS
DEFINITION
  1M0559N16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0559N16 F, genomic survey sequence.
ACCESSION
  AZ763729
VERSION
  AZ763729.1 GI:12875056
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
  ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
  and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
```


Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0559 row: N column: 16
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0559N16"
 /sex="Male"
 /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

7 a 3 c 3 g 6 t

Query Match 46.7%; Score 9.8; DB 28; Length 19;
 Best Local Similarity 84.6%; Pred. No. 8e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCTGATGAT 13
 |||||
 Db 5 AAGCATGACTGAT 17

RESULT 4

AZ504285/c

LOCUS

DEFINITION 1M0344J20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0344J20 F, genomic survey sequence.

ACCESSION

AZ504285

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0344 row: J column: 20

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES

source

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0344J20"
 /sex="Male"
 /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 5 c 2 g 7 t
 ORIGIN

Query Match 46.7%; Score 9.8; DB 28; Length 21;
 Best Local Similarity 84.6%; Pred. No. 8.4e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATTGATGACCAG 19
 |||||
 Db 21 GATTGATCATCAG 9

RESULT 5

C01992/c

LOCUS

DEFINITION

HUMS0004015 Human adult (K.Okubo) Homo sapiens cDNA, mRNA

sequence.

C01992

VERSION

C01992.1

KEYWORDS

EST.

SOURCE

Homo sapiens

(human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

Okubo,K.

BodyMap; human gene expression database

Unpublished

Contact: Okubo,K.

Institute for Molecular and Cellular Biol

Osaka University

1-3 Yamada-oka, Suita, Osaka Pref. 565, Japan

Tel: 06-877-5111(ex.3315)

Email: kousaku@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DDBJ

since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

FEATURES

source

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="adult"

/clone_lib="Human adult (K.Okubo)"

/notes="One or more human adult tissue"

6 a 5 c 4 g 4 t

BASE COUNT

ORIGIN

Query Match 44.8%; Score 9.4; DB 14; Length 19;

Best Local Similarity 90.9%; Pred. No. 1.2e+06;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCCTGATTGAT 13

|||||||

Db 12 GGCTGATTGAT 2

RESULT 6

AZ771145/c

LOCUS

DEFINITION 21 bp DNA linear GSS 16-FEB-2001

clone UUGC1M0573A09 F, genomic survey sequence.

ACCESSION

AZ771145

VERSION

AZ771145.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0573 row: A column: 09

Seq primer: CGTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0573A09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 6 c 3 g 10 t

ORIGIN

Query Match

Best Local Similarity 90.9%; Pred. No. 1.3e+06;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGCCTGATTGA 12

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Db 11 AGCCTGATTGA 1

RESULT 7

AZ509602/c

LOCUS

DEFINITION

21 bp DNA linear GSS 05-OCT-2000

clone UUGC1M0352E08 R, genomic survey sequence.

ACCESSION

AZ509602

VERSION

AZ509602.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0352 row: E column: 08

Seq primer: CACACAGGAACACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0352E08"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 4 c 5 g 6 t

ORIGIN

Query Match 43.8%; Score 9.2; DB 28; Length 21;
Best Local Similarity 78.6%; Pred. No. 1.6e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 ATTGATGACCAAGG 21

Db 18 ATTCAACACCAAGG 5

RESULT 8

AZ661528

LOCUS

DEFINITION 1M0540106F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 21)

Islam, H., Longacre, S., Mahmoud, M., Meenen, T., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0540 row: 1 column: 06

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0540106"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

FEATURES

source

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0542P18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 4 c 6 g 6 t

ORIGIN

Query Match 43.8%; Score 9.2; DB 28; Length 21;
Best Local Similarity 78.6%; Pred. No. 1.6e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCTGATGATGACC 17

Db 4 CTTAATGATGACC 17

RESULT 9

AZ662959

LOCUS

DEFINITION 1M0542P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 21)

Islam, H., Longacre, S., Mahmoud, M., Meenen, T., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0542 row: 1 column: 18

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0542P18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 5 c 2 g 7 t
ORIGIN

Query Match 43.8%; Score 9.2; DB 28; Length 21;
Best Local Similarity 78.6%; Pred. No. 1.6e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTGATTGATGACCA 18
|||||
Db 3 CTTATGATGACTA 16

RESULT 10
AZ774704
LOCUS
DEFINITION
2M004G18F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0004G18 F, genomic survey sequence.

ACCESSION
AZ774704
VERSION
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: G column: 18

Seq primer: CGTTGTAAACGACGCCAGT

Classes: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0004G18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

FEATURES
source

Query Match 41.9%; Score 8.8; DB 12; Length 16;
Best Local Similarity 83.3%; Pred. No. 2.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCTGATTGATG 14

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 6 c 2 g 5 t
ORIGIN

Query Match 43.8%; Score 9.2; DB 28; Length 21;
Best Local Similarity 78.6%; Pred. No. 1.6e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCTGATTGATGA 15
|||||
Db 1 AACCTCCTTGATGA 14

RESULT 11
BM395054/c

LOCUS

DEFINITION

50072-2-7-C10.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION
BM395054

VERSION
EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1. .16

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

5 a 5 c 4 g 2 t

BASE COUNT

ORIGIN

Query Match 41.9%; Score 8.8; DB 12; Length 16;
Best Local Similarity 83.3%; Pred. No. 2.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCTGATTGATG 14

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Db      14 GCCTGATGATG 3

RESULT 12
LOCUS   AZ987077/c
DEFINITION
2M0269H04R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0269H04 R, genomic survey sequence.
ACCESSION
AZ987077
VERSION
GSS
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
BASE COUNT      6 a      5 c      4 g      3 t      1 others
ORIGIN
1
|||||
14 GCCTGATGATG 3

Query Match      41.9%; Score 8.6; DB 14; Length 19;
Best Local Similarity 76.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCTGATGATG 14
|||
Db 17 ACCCTGTTGNTG 5

RESULT 13
LOCUS   AZ987077/c
DEFINITION
2M0269H04R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0269H04 R, genomic survey sequence.
ACCESSION
AZ987077
VERSION
GSS
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss

```

```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0269 row: H column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0269H04"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      5 a      3 c      5 g      8 t
ORIGIN
1
|||||
8 ATTGATGACCAG 19
|||||
21 ATTGATGACCAG 10

Query Match      41.9%; Score 8.8; DB 28; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.5e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATTGATGACCAG 19
|||||
Db 21 ATTGATGACCAG 10

RESULT 14
LOCUS   BQ594466
DEFINITION
E012442-024-024-J18-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-J18 5-PRIME, mRNA sequence.
ACCESSION
BQ594466
VERSION
BQ594466.1
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 18)
AUTHORS
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)

```

COMMENT

Contact: Weishaar B
ADIS DNA core facility at MPfZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpfz-koeln.mpg.de
Insert length: 18 Std Error: 0.00
Plate: 24 row: I column: 18
Seq primer: SP6; CATACGATTAGTGACACTAG.

FEATURES

source
1. 18
/organism="Beta vulgaris"
/mol_type="mrna"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="taxon:161934"
/clone="024-024-118"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-TV; Note:
Sequencing granted in the context of the GABI-Best project
local PI: Dr. Katharina Schneider, coordinator; Prof.
Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 3 a 3 c 9 g 3 t
ORIGIN

Query Match 41.0%; Score 8.6; DB 13; Length 18;
Best Local Similarity 73.3%; Pred. No. 2.9e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGCTGTGATTGATGA 15
| | | | |
Db 4 ACGCGTGGGTGATGA 18

RESULT 15

AZ307610 20 bp DNA linear GSS 29-SEP-2000
LOCUS IM0009G15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0009G15 R, genomic survey sequence.

ACCESSION AZ307610.1 GI:10346782
VERSION
KEYWORDS
SOURCE

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished

JOURNAL

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: G column: 15

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0009G15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 4 a 6 c 4 g 6 t
ORIGIN

Query Match 41.0%; Score 8.6; DB 28; Length 20;
Best Local Similarity 73.3%; Pred. No. 3e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GATTGATGACACGGG 21
| | | | |
Db 1 GATTCTCGACCATGTG 15

Search completed: February 20, 2004, 02:39:22

Job time : 1493 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 23:14:43 ; Search time 171 Seconds
(without alignments)
331.510 Million cell updates/sec

Title: US-10-085-108-21_COPY_711_731

Perfect score: 21

Sequence: 1 AAGCTGATGATGACCAAGG 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1588498

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq 19Jun03.*

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25: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	100.0	21	25	Human MAGE-C3 expr
C 2	12.8	61.0	19	16	H.pylori tox (-/-)
C 3	12.8	61.0	19	21	cdk3 ribozyme bind
C 4	12.8	61.0	19	21	cdk3 ribozyme bind
C 5	12.8	61.0	19	22	Cell-cycle depende
C 6	12.8	61.0	19	22	Cell-cycle depende
C 7	12.6	60.0	20	16	Primer B (Group 8,
C 8	12.6	60.0	21	19	Chicken matrix met

C 9	12.6	60.0	21	19	AAV12875	5' PCR primer used
C 10	12.6	60.0	21	22	AAF96809	Human gene single
C 11	12.4	59.0	15	17	AAT50147	Rabbit CERP HH rib
C 12	12.4	59.0	18	21	AAC64758	RRV PCR primer vmi
C 13	12.4	59.0	19	19	AAV08610	Primer ACE/188RT f
C 14	12.4	59.0	19	21	AAC61238	Primer ACE, AGT and
C 15	12.4	59.0	19	21	AAA38238	Human angiotensin-
C 16	12.4	59.0	20	19	AAV57869	Human chromosome 1
C 17	12.4	59.0	21	25	AAV51970	HGF RT-PCR primer
C 18	12.2	58.1	17	24	ABN08503	Human GDMPLP-1 17-m
C 19	12.2	58.1	17	24	ABN08504	Human GDMPLP-1 17-m
C 20	12.2	58.1	17	25	ABT38386	Tumour suppression
C 21	12.2	58.1	20	19	AAV57185	Human Notch-3 muta
C 22	12.2	58.1	20	24	AAD34914	Human E2F transcri
C 23	12.2	58.1	21	15	AAQ73414	Calcitonin recepto
C 24	12.2	58.1	21	25	AAD53380	Mouse bmf DNA spec
C 25	12	57.1	18	24	ABX15383	Human glyceraldehy
C 26	12	57.1	20	22	AAA91587	PCR primer for Hum
C 27	12	57.1	21	24	ABK82216	Human ATP-binding
C 28	12	57.1	21	25	AAD47337	Human RT-PCR rever
C 29	11.8	56.2	18	21	AAA86678	Cdc 2 kinase hamme
C 30	11.8	56.2	18	22	AAH61844	Cdc 2 kinase hamme
C 31	11.8	56.2	20	19	AAV20747	Human squalene epo
C 32	11.8	56.2	20	22	ABA82346	Zmaxi gene region
C 33	11.8	56.2	20	22	AAH56788	S. aureus groE ope
C 34	11.8	56.2	20	22	AAH56789	S. aureus groE ope
C 35	11.8	56.2	20	24	ABK23143	Human Zmaxi cDNA f
C 36	11.8	56.2	20	25	ACC45725	Human HEM SIS mark
C 37	11.8	56.2	21	15	AAQ71069	Primer #1 for ampl
C 38	11.6	55.2	18	18	AAT91792	Primer DET643 for
C 39	11.6	55.2	19	14	AAQ51831	bcr mRNA ribozyme
C 40	11.6	55.2	20	16	AAQ75163	RAR-beta-1/beta-3
C 41	11.6	55.2	20	18	AAT66286	Primer 30 for hop
C 42	11.6	55.2	20	20	AAX59763	Primer P2 used to
C 43	11.6	55.2	20	21	AAZ92612	Primer 4, a murine
C 44	11.6	55.2	20	22	AAF89928	PCR primer used to
C 45	11.6	55.2	20	24	AAD29426	Human BMPR2 exon1

ALIGNMENTS

RESULT 1

ABX95022/c
ID ABX95022 standard; DNA; 21 BP.

XX ABX95022;

XX ABX95022;

DT 05-JUN-2003 (first entry)

XX Human MAGE-C3 expression pattern anlalysis RT-PCR antisense primer.

XX TRAP; ss; tumour rejection antigen precursor; cytolytic T-cell; CTL;

XX tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor;

XX head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma;

XX cutaneous melanoma; nonsmall cell lung cancer; MAGE-C3;

XX human; reverse transcription.

XX Homo sapiens.

XX US2002176865-A1.

XX 28-NOV-2002.

XX 01-MAR-2002; 2002US-0085108.

XX 09-FEB-2000; 2000US-0501104.

XX 25-APR-1997; 97US-0845528.

XX 24-APR-1998; 98US-0066281.

XX 17-DEC-1999; 99US-0468433.

XX (LUCA/) LUCAS S.

XX (BOON/) BOON-FALLEUR T.

XX Lucas S, Boon-Falleur T;
 XX WPI; 2003-328468/31.
 XX Novel isolated nucleic acid encoding tumor rejection antigen precursor
 PT MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine
 PT presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or
 PT MAGE-B6
 XX
 XX Example 12; Page 13; 59pp; English.
 XX The invention relates to an isolated nucleic acid molecule which encodes
 CC a tumor rejection antigen precursor (TRAP) having an amino acid sequence
 CC of a TRAP encoded by a fully defined MAGE-C3, MAGE-B5, or MAGE-B6
 CC polynucleotide sequence. Also disclosed is a method which is useful for
 CC determining presence of cytolytic T-cells specific for complexes of human
 CC leukocyte antigen (HLA) and a peptide derived from the nucleic acid in a
 CC cytotoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is
 CC useful as a diagnostic probe to determine the presence of abnormal
 CC (tumour) cells such as seminoma, bladder transitional-cell carcinoma,
 CC head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma,
 CC cutaneous melanoma or non-small cell lung cancer (NSCLC) which express
 CC MAGE-C1, MAGE-B5 or MAGE-B6. The nucleic acid is useful for diagnosing a
 CC disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPS
 CC or tumour rejection antigens (TRAs). The present sequence represents the
 CC human MAGE-C3 expression pattern anlaysis reverse transcription (RT)-PCR
 CC antisense primer.
 XX
 XX Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
 SQ
 Query Match 100.0%; Score 21; DB 25; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.39; 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCTGATTGATGACACAGG 21
 Db 21 AAGCTGATTGATGACACAGG 1
 RESULT 2
 AAT04143
 ID AAT04143 standard; DNA; 19 BP.
 XX
 AC AAT04143;
 XX
 DT 19-APR-1996 (first entry)
 XX
 DE H.pylori tox (+/-) vacA gene amplification primer 6.
 XX
 KW Vacuolating toxin; vaccine; immunisation; therapy; mutant; infection;
 KW Helicobacter pylori; PCR; primer; amplification; ss.
 XX
 OS Synthetic.
 OS
 PN WO9522988-A1.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-US02219.
 XX
 PR 23-FEB-1994; 94US-0200232.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Blaser MJ, Cover TL;
 XX
 XX WPI; 1995-311383/40.
 DR Isolated DNA encoding Helicobacter pylori vacuolating toxin - useful
 XX for immunisation against H. pylori infection
 XX Examples; Page 31; 64pp; English.
 PS

XX Nucleic acid encoding the Helicobacter pylori vacuolating toxin
 CC (AAT01432) and a genetically altered mutant strain of H. pylori which
 CC contains a foreign nucleic acid and does not express a functional
 CC vacuolating toxin may be used to immunise a subject against H.pylori
 CC infection. They may possibly also be used therapeutically.
 CC The primers AAT04140-5 were used to amplify and compare fragments of the
 CC vacuolating toxin coding sequence vacA from tox(+) and tox(-) strains of
 CC H.pylori. The primers AAT04142-3 amplified a 0.6 kb region from the
 CC downstream portion of the gene in each of the strains tested.
 XX
 XX Sequence 19 BP; 5 A; 5 C; 3 G; 6 T; 0 other;
 SQ
 Query Match 61.0%; Score 12.8; DB 16; Length 19;
 Best Local Similarity 87.5%; Pred. No. 6e+03; 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAGCTGATTGATGAC 16
 Db 1 AAGCTGATTGATGAC 16
 RESULT 3
 AA82757/C
 ID AA82757 standard; DNA; 19 BP.
 XX
 AC AA82757;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE cdk3 ribozyme binding site #42.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KW restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO2000032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28772.
 XX
 PR 04-DEC-1998; 98US-0110954.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 XX WPI; 2000-412314/35.
 DR New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -
 XX
 PS Disclosure; Page 51; 109pp; English.
 XX
 CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX
 XX Sequence 19 BP; 6 A; 5 C; 4 G; 4 T; 0 other;
 SQ
 Query Match 61.0%; Score 12.8; DB 21; Length 19;
 Best Local Similarity 87.5%; Pred. No. 6e+03; 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 CTGATTGATGACACAGG 20

XX WO9745137-A1.
 XX
 XX
 PD 04-DEC-1997.
 XX
 XX 30-MAY-1997; 97WO-US09158.
 XX
 XX 31-MAY-1996; 96US-0018733.
 PR 31-MAY-1996; 96US-0015869.
 XX
 XX (SCRI) SCRIPPS RES INST.

PA Brooks P, Cheres DA, Friedlander M;
 XX WPI; 1998-041758/04.
 XX
 XX Packaging material containing polypeptide antagonist of alphav,
 PT beta3 integrin - used for inhibition of angiogenesis, and for
 PT treating tumours, inflammation, eye diseases etc.
 XX
 XX Example 4; Page 59; 234pp; English.

XX This 5' primer corresponds to nucleotides 809-830 of the chicken
 CC matrix metalloproteinase-2 (chMMP-2) mature polypeptide coding
 CC region (see AAV03995). It was used with a 3' primer (see AAV03996)
 CC to amplify a portion of coding region encoding amino acids
 CC 274-637 of chMMP-2. The 5' primer was designed to incorporate a
 CC BamHI site allowing directional ligation of the amplified product
 CC into pGEX-lambda or pGEX-3X expression vectors. Recombinant
 CC chMMP-2 (274-637) was expressed as a fusion protein with
 CC glutathione-S-transferase in E. coli transformants. The invention
 CC relates to the discovery that angiogenesis is mediated by the
 CC specific vitronectin receptor alpha-v beta-3, and that inhibition
 CC of alpha-v beta-3 function inhibits angiogenesis. Claimed
 CC antagonists of alpha-v beta-3 include C-terminal fragments (see
 CC AAW41083-94) of human or chicken MMP-2 and fusion proteins.
 XX
 XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;
 SQ

Query Match 60.0%; Score 12.6; DB 19; Length 21;
 Best Local Similarity 78.9%; Pred. No. 7.8e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCTGATTGATGACCAAGG 21
 |||||
 Db 1 GCCGGATCCATGACCAAGT 19

RESULT 9
 AAV12875
 ID AAV12875 standard; DNA; 21 BP.
 XX
 XX AAV12875;
 AC

DT 09-JUN-1998 (first entry)

XX 5' PCR primer used to obtain cDNA encoding chicken MMP-2 fragments.
 XX Metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation; PCR primer; ss.
 XX Synthetic.
 OS Gallus sp.
 OS

XX WO9745447-A1.
 PN
 XX
 XX 04-DEC-1997.
 PD
 XX 30-MAY-1997; 97WO-US09099.
 XX
 XX 31-MAY-1996; 96US-0018733.
 PR 31-MAY-1996; 96US-0015869.
 PR

XX (SCRI) SCRIPPS RES INST.
 XX Brooks P, Cheres DA, Friedlander M;
 XX WPI; 1998-041758/04.
 XX
 XX Packaging material containing polypeptide antagonist of alphav,
 PT beta5 integrin - used for inhibition of angiogenesis, and for
 PT treating tumours, inflammation, eye diseases etc.
 XX
 XX Example 7; Page 57; 117pp; English.

XX PCR primers AAV12874-78 were used, together with AAV12873 as the 3'
 CC primer, to obtain cDNA encoding chicken matrix metalloproteinase-2 (MMP-2)
 CC protein fragments (AAW41234-39). Fragments of the MMP-2 protein act as
 CC alpha-v-beta-5 antagonists. Alpha-v-beta-5 is a vitronectin receptor.
 CC Inhibitors of alpha-v-beta-5 can inhibit angiogenesis. The specification
 CC describes a novel labelled package that contains an inhibitor of
 CC angiogenesis i.e. an alpha-v-beta-5 antagonising polypeptide that binds
 CC to integrin alpha-v-beta-5 and includes a part of the C-terminal domain
 CC of MMP-2. The antagonists are used to inhibit angiogenesis in inflamed
 CC tissue, in solid tumours or metastases, and in a wide range of ocular
 CC disorders (e.g. diabetic or other forms of retinopathy, neovascular
 CC glaucoma, or corneal transplants). They are particularly used to induce
 CC regression or to inhibit growth of tumours. The alpha-v-beta-5
 CC antagonists can also be used to treat restenosis caused by migration of
 CC smooth muscle cells following angioplasty and to reduce blood supply to
 CC selected tissues. The antagonists particularly inhibit
 CC neovascularisation where this is induced by cytokines, e.g. transforming
 CC growth factor alpha, epidermal growth factor or especially vascular
 CC endothelial growth factor.

XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;
 SQ

Query Match 60.0%; Score 12.6; DB 19; Length 21;
 Best Local Similarity 78.9%; Pred. No. 7.8e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCTGATTGATGACCAAGG 21
 |||||
 Db 1 GCCGGATCCATGACCAAGT 19

RESULT 10
 AAF96809/c
 ID AAF96809 standard; DNA; 21 BP.
 XX
 XX AAF96809;
 AC

DT 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #1570.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 FH replace(11,G)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 FT

XX WO200118250-A2.
 PN
 XX
 XX 15-MAR-2001.
 PD
 XX 07-SEP-2000; 2000WO-US24503.
 PF
 XX 10-SEP-1999; 99US-0153357.
 PR

```

PR 26-JUL-2000; 2000US-0220947.
PR 16-AUG-2000; 2000US-0225724.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis -
XX
XX Examples; Page 153; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism
XX and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification.
XX
XX Sequence 21 BP; 6 A; 9 C; 5 G; 1 T; 0 other;
XX
XX
XX Query Match 60.0%; Score 12.6; DB 22; Length 21;
XX Best Local Similarity 78.9%; Pred. No. 7.8e+03;
XX Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 3 GCCTGATTGATGACCACGG 21
XX ||||| ||||| |||||
XX 20 GCTGCGGTGTGACCTGG 2
XX
XX
XX RESULT 11
XX AAT50147/c
XX ID AAT50147 standard; RNA; 15 BP.
XX
XX AC AAT50147;
XX
XX XX 07-MAR-1997 (first entry)
XX
XX XX Rabbit CPTP HH ribozyme target sequence #330.
XX
XX XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; athrectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CPTP;
XX familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
XX LDL; 55.
XX
XX XX Oryctolagus cuniculus.
XX
XX XX WO9620279-A1.
XX
XX XX 04-JUL-1996.
XX
XX XX 11-DEC-1995; 95WO-US16000.
XX
XX XX 23-DEC-1994; 94US-0363240.
XX
XX XX (RIBO-) RIBOZYME PHARM INC.
XX XX (WARN ) WARNER LAMBERT CO.
XX
XX Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
XX

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DR	WPI; 1996-321852/32.
PT	New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT	- useful for preventing or treating initial development, progression
PT	or regression of vascular diseases, esp. familial
PT	hypercholesterolaemia
XX	
PS	Claim 4; Page 40; 72pp; English.
XX	
CC	AA750138-750359 represent target sequences for the rabbit cholesterol
CC	ester transfer protein (CETP) hamsterhead (HH) ribozymes (see
CC	AA750360-750546). CETP is a 74 kD glycoprotein that facilitates neutral
CC	lipid transfer between plasma lipoproteins. The numbering of the targets
CC	refers to the position of the cleavage site in full length CETP. The
CC	ribozyme then binds to 5 nucleotides either side of this site. The
CC	ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
CC	blocking synthesis and/or expression of the mRNA. By inhibiting CETP,
CC	the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC	eliminated) thereby preventing the reduction in size density of the high
CC	density lipoproteins (HDL), prolonging HDL half life, and therefore
CC	increasing HDL levels. The ribozymes can be used to treat conditions
CC	associated with abnormal levels of CETP, specifically atherosclerosis,
CC	familial hypercholesterolaemia, peripheral vascular disease,
CC	dyslipidaemia, hyperbetalipoproteinaemia, hypopalipoproteinaemia,
CC	vascular complications of diabetes, transplant, atherectomy and
CC	angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC	density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC	(a decrease in LDL levels, and a corresponding increase in HDL levels).
CC	The HH ribozymes can also be used diagnostically to study genetic drift
CC	and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC	ribozymes target specific regions of the CETP gene, they have low
CC	non-specific activity.
XX	
SQ	Sequence 15 BP; 4 A; 3 C; 4 G; 4 U; 0 other;
	Query Match 59.0%; Score 12.4; DB 17; Length 15;
	Best Local Similarity 92.9%; Pred. No. 9.2e+03;
	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy	5 CTGATTGATGACCA 18
Db	14 CTGATTGATGCCCA 1
RESULT 12	
AC664758/c	
ID AAC64758	standard; DNA; 18 BP.
XX AAC64758;	
XX AAC64758;	
XX AAC64758;	
DT 28-FEB-2001	(first entry)
XX	
XX	
DE RRV PCR primer vMIP-2	SRQ ID NO:167.
XX	
KW Macaca mulatta rhadinovirus 17577;	RRV; rhesus macaque rhadinovirus;
KW genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;	
KW IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;	
KW cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;	
KW lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;	
KW splenomegaly; hypergammaglobulinemia; autoimmune haemolytic anaemia;	
KW PCR primer; ss.	
XX	
OS Macaca mulatta rhadinovirus 17577.	
XX	
XX	
PN WO200028040-A2.	
XX	
PD 18-MAY-2000.	
XX	
XX	
PF 05-NOV-1999;	99WO-US26260.
XX	
PR 06-NOV-1998;	98US-0107507.
XX	
PR 20-NOV-1998;	98US-0109409.
XX	

PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Wong SW, Axthelm MK, Searles RP;
 XX
 DR WPI; 2000-376552/32.
 XX
 PT New rhesus rhadino virus for producing non-human primate model useful
 PT for testing potential treatments and efficacy of the candidate vaccine
 PT for conditions associated with RRV infection -
 XX
 PS Example 13; Page 34; 141pp; English.
 XX
 CC The present invention describes a novel rhesus macaque rhadinovirus
 CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
 CC RRV genome sequence, and AAB53204 represent the proteins
 CC encoded by the genome sequence. The present invention also specifically
 CC claims the individual open reading frame (ORF) nucleotide sequences from
 CC the genome which encode the individual proteins, but these sequences are
 CC not given. A non-human animal infected with RRV can be used for testing
 CC the efficacy of drug in the treatment of condition associated with
 CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative
 CC disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
 CC hypergammaglobulinemia or autoimmune haemolytic anaemia, by
 CC administering the drug to a immuno-compromised non-human primate
 CC preferably Rhesus macaque monkey obtained by as a result of infection
 CC by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
 CC non-human primate model for testing potential treatments for conditions
 CC associated with RRV infection. It is also useful for testing the
 CC efficacy of the candidate vaccine against RRV infection or conditions
 CC associated with its infection by administering the vaccine to the
 CC subject capable of infection with RRV, inoculating the subject with RRV
 CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
 CC to AAB53213 represent sequence used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 18 BP; 4 A; 5 C; 5 G; 4 T; 0 other;
 XX
 Query Match 59.0%; Score 12.4; DB 21; Length 18;
 Best Local Similarity 92.9%; Pred. No. 9.6e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AGCCTGATTGATGA 15
 DB 15 AGCCTGATTGACGA 2
 XX
 RESULT 13
 ID AAV08610 standard; DNA; 19 BP.
 XX
 AC AAV08610;
 XX
 DT 15-FEB-1999 (first entry)
 DE Primer ACE/188RT for human ACE gene.
 XX
 KW PCR primer; human; ACE; angiotensin converting enzyme; angiotensinogen;
 KW cardiovascular status; AGT; ATI; type 1 angiotensin II receptor; stroke;
 KW polymorphic pattern; blood pressure; electrocardiographic profile;
 KW cardiac condition diagnosis; myocardial infarction; atherosclerosis;
 KW hypertension; cardiovascular disease; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9845477-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 01-APR-1998; 98WO-IB00475.
 XX
 PR 04-APR-1997; 97US-0042930.
 XX

PA (EURO-) EURONA MEDICAL AB.
 XX
 PI Andersson MK, Lindstroem PHR, Norberg LT;
 XX
 DR WPI; 1998-568361/48.
 XX
 PT Assessing cardiovascular status in humans by polymorphic analysis -
 PT of genes for angiotensin converting enzyme, angiotensinogen and
 PT angiotensin II receptor, used to diagnose predisposition to disease
 PT and to predict of therapy
 XX
 PS Example 1; Page 28; 71pp; English.
 XX
 CC This sequence represents a PCR primer for the human ACE (angiotensin
 CC converting enzyme) gene, and can be used in the method of the invention.
 CC The method is for assessing cardiovascular status in humans by
 CC determining the sequence of at least one polymorphic site in the ACE
 CC (angiotensin converting enzyme), AGT (angiotensinogen) and/or ATI (type 1
 CC angiotensin II receptor) genes, and comparing the polymorphic pattern
 CC with that in patients with predetermined markers of status. The method is
 CC used to assess blood pressure or electrocardiographic profile, to
 CC diagnose a cardiac condition such as (silent) myocardial infarction (MI),
 CC hypertension, atherosclerosis or stroke. They can also be used to predict
 CC response to treatments with ACE inhibitors, angiotensin II receptor
 CC antagonists, diuretics, alpha- or beta-adrenergic receptor
 CC antagonists, etc. It is also used to identify susceptibility to
 CC cardiovascular disease. Libraries of nucleic acids containing polymorphic
 CC positions in the 3 genes, and libraries of targets corresponding to the
 CC peptides from the genes are used to screen for cardiovascular agents. The
 CC nucleic acids contained in the library can be used as source of
 CC probes.
 XX
 SQ Sequence 19 BP; 3 A; 3 C; 8 G; 5 T; 0 other;
 XX
 Query Match 59.0%; Score 12.4; DB 19; Length 19;
 Best Local Similarity 92.9%; Pred. No. 9.7e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AGCCTGATTGATGA 15
 DB 4 AGCCTGGTGTGATGA 17
 XX
 RESULT 14
 ID AAC61238 standard; DNA; 19 BP.
 XX
 AC AAC61238;
 XX
 DT 30-JAN-2001 (first entry)
 DE Human ACE, AGT and ATI genes polymorphisms PCR primer SEQ ID NO: 38.
 XX
 KW Human; genetic polymorphism; disease diagnosis; treatment; cancer;
 KW cardiovascular system; nervous system; glaucoma; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS WO2000056922-A2.
 XX
 PN 28-SEP-2000.
 PD 23-MAR-2000; 2000WO-GB01102.
 XX
 PR 23-MAR-1999; 99US-0126046.
 PR 23-MAR-1999; 99WO-IB00497.
 PR 24-MAR-1999; 99US-0126243.
 PR 23-DEC-1999; 99US-0471890.
 XX
 PA (GEMI-) GEMINI GENOMICS AB.
 XX
 PI Lindstrom PHR, Norberg LT, Jonsson L, Olaisson E, Sanders R;
 XX

DR WPI; 2000-638268/61..

XX Assessing disease status in individual by determining sequence(s) at

PT one or more polymorphic positions within the human genes encoding the

PT protein(s) involved in physiological pathway associated with treatment

PT regime -

XX Example 1; Page 57; 141pp; English.

XX The present invention is related to methods for determining the

CC polymorphic pattern of an individual and using the results to determine

CC their risk of a number of diseases, including cancer, cardiovascular

CC diseases, glaucoma and nervous system disorders such as depression and

CC neurodegenerative diseases. In addition, the methods can be used to

CC determine the effects of different types of treatment for individuals,

CC and thus enables appropriate therapies to be prescribed. The PCR primers

CC shown in sequences AAC61201-C61371 were all used to demonstrate the

CC methods of the invention.

XX Sequence 19 BP; 3 A; 3 C; 8 G; 5 T; 0 other;

SQ

Query Match 59.0%; Score 12.4; DB 21; Length 19;

Best Local Similarity 92.9%; Pred. No. 9.7e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGCCTGATTGATGA 15

Db ||||| |||||

4 AGCCTGGTTGATGA 17

RESULT 15

AAA38238

ID AAA38238 standard; DNA; 19 BP.

XX AC AAA38238;

XX 21-AUG-2000 (first entry)

XX Human angiotensin-converting enzyme (ACE) PCR primer, SEQ ID NO:38.

XX Angiotensin-converting enzyme gene; ACE; polymorphism;

KW polymorphic marker; cardiovascular disease; myocardial infarction;

KW unstable angina; hypertension; atherosclerosis; stroke; prognosis;

KW drug screening; treatment outcome; human; PCR primer; ss.

XX Homo sapiens.

XX WC2000022166-A2.

XX 20-APR-2000.

XX 13-OCT-1999; 99WO-IB01678.

XX 14-OCT-1998; 98US-0104286.

PR 14-OCT-1998; 98US-0104302.

XX (EURO-) EURONA MEDICAL AB.

XX Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;

XX WPI; 2000-318010/27.

XX Assessing cardiovascular status in humans involves comparing test

PT polymorphic pattern comprising polymorphic positions within genes

PT encoding specific proteins, with reference polymorphic pattern -

XX Example 1; Page 49; 126pp; English.

XX The invention relates to a novel method of assessing the cardiovascular

CC status in an individual and to newly identified polymorphisms in the

CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II

CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,

CC aldosterone synthase, endothelin receptor type A and beta-adrenergic

CC receptors 1 and 2. The method comprises determining the sequence at one

CC or more polymorphic positions within these genes, and comparing the

CC pattern of polymorphisms from the individual with a reference

CC polymorphic pattern obtained from a population of individuals exhibiting

CC a predetermined cardiovascular disease status. The polymorphic markers

CC are useful for determining the predisposition of an individual to

CC cardiovascular disorders such as myocardial infarction, unstable angina,

CC hypertension, atherosclerosis and stroke. They are also useful for

CC predicting the likely cardiovascular status of a patient given a

CC treatment regimen comprising administration of cardiovascular drugs

CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers

CC provides a basis for predicting the outcome of a treatment regimen.

CC Fragments of the genes comprising a polymorphic site may be used as

CC primers and probes for detecting genetic polymorphisms or in molecular

CC library arrays for high throughput screening. The genes, and the

CC proteins they encode are useful in the screening of potential

CC cardiovascular drugs. Determination of an individual's polymorphic

CC pattern reduces or eliminates trial and error in selecting a treatment

CC for a particular individual cardiovascular patient. It also provides the

CC ability to eliminate patients from clinical trials who are predicted to

CC be non-responsive, or at a risk for an adverse response, to a particular

CC treatment regimen. Adverse results in an early trial can be evaluated to

CC identify polymorphic patterns so that the adverse results can be

CC correlated with a sub-population of the test population, permitting

CC exclusion of such sub-populations from the treatment group. Beneficial

CC drugs can be approved for use in the appropriate population, thereby

CC decreasing the number of patients required for a clinical trial, which

CC in turn decreases the duration and cost of such trials. Sequences

CC AAA38201-A38239 represent PCR primers used in an exemplification of

CC the invention to amplify short fragments of the human ACE gene

CC (AAA38328- AAA38330) for sequence determination.

XX

SQ Sequence 19 BP; 3 A; 3 C; 8 G; 5 T; 0 other;

Query Match 59.0%; Score 12.4; DB 21; Length 19;

Best Local Similarity 92.9%; Pred. No. 9.7e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGCCTGATTGATGA 15

Db ||||| |||||

4 AGCCTGGTTGATGA 17

Search completed: February 20, 2004, 00:55:58

Job time : 172 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 23:16:19 ; Search time 1597.5 Seconds
(without alignments)
537.779 Million cell updates/sec

Title: US-10-085-108-21_COPY_711_731

Perfect score: 21

Sequence: 1 AAGCCTGATTGATGACCAGG 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 637448

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

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13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

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18: em.in.*

19: em.mu.*

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32: em.htg.mus.*

33: em.htg.pln.*

34: em.htg.rod.*

35: em.htg.mam.*

36: em.htg.vrt.*

37: em.sy.*

38: em.htgo.hum.*

39: em.htgo.mus.*

40: em.htgo.other.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	12.8	61.0	19	6	AX129125	AX129125 Sequence
C 2	12.8	61.0	19	6	AX129126	AX129126 Sequence
C 3	12.8	61.0	19	6	I89405	I89405 Sequence 16
C 4	12.6	60.0	21	6	AR269340	AR269340 Sequence
C 5	12.6	60.0	21	6	AX096396	AX096396 Sequence
C 6	12.4	59.0	19	6	AR137291	AR137291 Sequence
C 7	12.4	59.0	19	6	AX037413	AX037413 Sequence
C 8	12.4	59.0	19	6	BD075165	BD075165 Methods f
C 9	12.4	59.0	20	6	AR233464	AR233464 Sequence
C 10	12.2	58.1	17	6	AX732389	AX732389 Sequence
C 11	12.2	58.1	17	6	AX735038	AX735038 Sequence
C 12	12.2	58.1	20	6	AR225911	AR225911 Sequence
C 13	12	57.1	20	6	AX134104	AX134104 Sequence
C 14	12	57.1	20	6	AX189713	AX189713 Sequence
C 15	12	57.1	21	6	AX553656	AX553656 Sequence
C 16	12	57.1	21	6	BD142983	BD142983 Method of
C 17	11.8	56.2	17	6	AX735886	AX735886 Sequence
C 18	11.8	56.2	18	6	AX133050	AX133050 Sequence
C 19	11.8	56.2	20	6	AX148051	AX148051 Sequence
C 20	11.8	56.2	20	6	AX149234	AX149234 Sequence
C 21	11.8	56.2	20	6	AX149235	AX149235 Sequence
C 22	11.8	56.2	21	4	DOGE21302	LI5691 dog (Clone:
C 23	11.8	56.2	21	6	AR098872	AR098872 Sequence
C 24	11.8	56.2	21	6	AR275185	AR275185 Sequence
C 25	11.8	56.2	21	6	I79712	I79712 Sequence 7
C 26	11.6	55.2	19	6	A87308	A87308 Sequence 33
C 27	11.6	55.2	19	6	BD057386	BD057386 Protein c
C 28	11.6	55.2	19	6	I83633	I83633 Sequence 7
C 29	11.6	55.2	20	6	A95470	A95470 Sequence 20
C 30	11.6	55.2	20	6	AR072824	AR072824 Sequence
C 31	11.6	55.2	20	6	AR177533	AR177533 Sequence
C 32	11.6	55.2	20	6	AX135802	AX135802 Sequence
C 33	11.6	55.2	20	6	AX375541	AX375541 Sequence
C 34	11.6	55.2	21	6	AR100947	AR100947 Sequence
C 35	11.6	55.2	21	6	AR240235	AR240235 Sequence
C 36	11.4	54.3	15	6	AX635907	AX635907 Sequence
C 37	11.4	54.3	15	6	AX636096	AX636096 Sequence
C 38	11.4	54.3	15	6	I61477	I61477 Sequence 31
C 39	11.4	54.3	15	6	I61666	I61666 Sequence 22
C 40	11.4	54.3	17	6	AX733387	AX733387 Sequence
C 41	11.4	54.3	20	6	AX188466	AX188466 Sequence
C 42	11.4	54.3	20	6	E32494	E32494 Primer for
C 43	11.4	54.3	21	6	AX675050	AX675050 Sequence
C 44	11.4	54.3	21	6	BD088558	BD088558 A method
C 45	11.4	54.3	21	12	AB069455	AB069455 Synthetic

ALIGNMENTS

RESULT 1	AX129125/c	AX129125	19 bp	DNA	linear	PAT 15-MAY-2001
LOCUS	Sequence 343 from Patent WO0130362.					
DEFINITION	AX129125					
ACCESSION	AX129125					
VERSION	AX129125.1	GI:14135430				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.					
TITLE	Robbins, J.M. and Tritz, R.					
	Ribozyme therapy for the treatment of proliferative skin and eye					
	diseases					

JOURNAL Patent: WO 0130362-A 343 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1. 19
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="cdk3 ribozyme binding site"
BASE COUNT 6 a 5 c 4 g 4 t
ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTGATTGATGACCGAG 20
Db 19 CTCATTGATGACCGAG 4

RESULT 2
AX129126/c
LOCUS AX129126 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 344 from Patent WO0130362.
ACCESSION AX129126
VERSION AX129126.1 GI:14135431
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE 1
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 344 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
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1. 19
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="cdk3 ribozyme binding site"
BASE COUNT 4 a 5 c 4 g 6 t
ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTGATTGATGACCGAG 20
Db 16 CTCATTGATGACCGAG 1

RESULT 3
I89405
LOCUS I89405 19 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 16 from patent US 5721349.
ACCESSION I89405
VERSION I89405.1 GI:3409345
KEYWORDS
SOURCE Unknown.
ORGANISM

REFERENCE 1 (bases 1 to 19)
AUTHORS Cover, T.L. and Blaser, M.J.
TITLE Vacuolating toxin-deficient *H. pylori*
JOURNAL Patent: US 5721349-A 16 24-FEB-1998;
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1. 19
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BASE COUNT 5 a 5 c 3 g 6 t

ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGAC 16
Db 1 AAGCTTGATTGATGAC 16

RESULT 4
AR269340
LOCUS AR269340 21 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 33 from patent US 6500924.
ACCESSION AR269340
VERSION AR269340.1 GI:29700458
KEYWORDS
SOURCE Unknown.
ORGANISM

REFERENCE 1 (bases 1 to 21)
AUTHORS Brooks, P.C., Cheresch, D.A. and Silletti, S.A.
TITLE Methods and compositions useful for inhibition of angiogenesis
JOURNAL Patent: US 6500924-A 33 31-DEC-2002;
FEATURES
source
1. 21
/organism="unknown"
BASE COUNT 5 a 6 c 6 g 4 t
ORIGIN

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Best Local Similarity 78.9%; Pred. No. 2.9e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCTGATTGATGACCGAG 21
Db 1 GCCGGATCCATGACCGAGT 19

RESULT 5
AX096396/c
LOCUS AX096396 21 bp DNA linear PAT 31-MAR-2001
DEFINITION Sequence 1574 from Patent WO0118250.
ACCESSION AX096396
VERSION AX096396.1 GI:13512650
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE 1
AUTHORS Lander, E.S., Gargill, M., Ireland, J.S., Bolck, S., Daley, G.Q. and McCarthy, J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1574 15-MAR-2001;
WHITHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1. 21
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 9 c 5 g 1 t 1 others
ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 2.9e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCTGATTGATGACCGAG 21
Db 20 GCCTGCGTGTGACCTGG 2

DEFINITION Methods for assessing cardiovascular status and compositions for use thereof.

RESULT 6
ARI137291
LOCUS ARI137291 19 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 38 from patent US 6197505.
ACCESSION ARI137291
VERSION ARI137291.1 GI:14478800
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Norberg,L.T., Olaisson,E., Jonsson,L., Lindstrom,P.H. and
Lindstrom,P.Harry,Rutger.
TITLE Methods for assessing cardiovascular status and compositions for
use thereof
JOURNAL Patent: US 6197505-A 38 06-MAR-2001;
FEATURES Location/Qualifiers
source 1..19
BASE COUNT 3 a 3 c 8 g 5 t
ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 19;
Best Local Similarity 92.9%; Pred. No. 3.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 AGCCTGATTGATGA 15
Db 4 AGCCTGGTTGATGA 17

RESULT 7
AX037413
LOCUS AX037413 19 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 38 from Patent WO0056922.
ACCESSION AX037413
VERSION AX037413.1 GI:11226838
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Norberg,L.T., Olaisson,E., Jonsson,L., Lindstrom,P.H. and
Sanders,R.
TITLE Genetic polymorphism and polymorphic pattern for assessing disease
status, and compositions for use thereof
JOURNAL Patent: WO 0056922-A 38 28-SEP-2000;
NORBERG LEIF TORBJORN (SE) ; OLAISSON ERIK (SE) ; JONSSON LENA (SE)
; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ;
SANDERS RHANNON (SE)
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

BASE COUNT 3 a 3 c 8 g 5 t
ORIGIN
Query Match 59.0%; Score 12.4; DB 6; Length 19;
Best Local Similarity 92.9%; Pred. No. 3.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 AGCCTGATTGATGA 15
Db 4 AGCCTGGTTGATGA 17

RESULT 8
BD075165
LOCUS BD075165 19 bp DNA linear PAT 27-AUG-2002

DEFINITION Methods for assessing cardiovascular status and compositions for use thereof.

ACCESSION BD075165
VERSION BD075165.1 GI:22620768
KEYWORDS JP 2001519660-A/38.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Norberg,L.T., Andersson,M.K. and Lindstrom,P.H.R.
TITLE Methods for assessing cardiovascular status and compositions for use thereof
JOURNAL Patent: JP 2001519660-A 38 23-OCT-2001;
COMMENT OS Artificial Sequence
PN JP 2001519660-A/38
PD 23-OCT-2001
PF 01-APR-1998 JP 1998542530
PI 04-APR-1997 US 60/042930
PI LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM
PC C1201/68,C07K14/72,C07K14/575,C12N9/48
CC Description of Artificial Sequence: PCR PRIMER FH Key
FEATURES Location/Qualifiers
FT source 1..19
FT /organism='Artificial Sequence'.
source Location/Qualifiers
1..19
/organism="synthetic construct"
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/db_xref="taxon:32630"

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGCCTGATTGATGA 15
Db 4 AGCCTGGTTGATGA 17

RESULT 9
AR233464
LOCUS AR233464 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 93 from patent US 6458532.
ACCESSION AR233464
VERSION AR233464.1 GI:27276055
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Detera-Wadleigh,S.D., Yoshikawa,T., Sanders,A.R. and Esterling,L.E.
TITLE Polynucleotides encoding IMP 18p myo-inositol monophosphatase and
methods of detecting said polynucleotides
JOURNAL Patent: US 6458532-A 93 01-OCT-2002;
FEATURES Location/Qualifiers
source 1..20
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BASE COUNT 5 a 2 c 9 g 4 t
ORIGIN

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Best Local Similarity 92.9%; Pred. No. 3.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2 GATTGAGGACCAGG 15

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RESULT 10
AX732389/c
LOCUS AX732389 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4023 from Patent WO03025175.
ACCESSION AX732389
VERSION AX732389.1 GI:30511732
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
source Telerman,A., Amson,R. and Tuijnder,M.
Patent: WO 03025175-A 4023 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 6 a 4 c 4 g 3 t
ORIGIN
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Best Local Similarity 82.4%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGCCTGATTGATGACC 17
Db 17 ATGCTGATGCTGATC 1

RESULT 11
AX735038/c
LOCUS AX735038 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 628 from Patent WO03025177.
ACCESSION AX735038
VERSION AX735038.1 GI:30514315
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
source Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
Patent: WO 03025177-A 628 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1. .17
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BASE COUNT 6 a 4 c 4 g 3 t
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Query Match 58.1%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGCCTGATTGATGACC 17
Db 17 ATGCTGATGCTGATC 1

RESULT 12
AR225911/c
LOCUS AR225911 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 15 from Patent WO0148240.
ACCESSION AX189713
VERSION AX189713.1 GI:15143089
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
source Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
Patent: WO 03025177-A 628 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Query Match 58.1%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 17 ATGCTGATGCTGATC 1

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DEFINITION Sequence 61 from patent US 6444464.
ACCESSION AR225911
VERSION AR225911.1 GI:27264065
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt,J.
TITLE Antisense modulation of E2F transcription factor 2 expression
JOURNAL Patent: US 6444464-A 61 03-SEP-2002;
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source Location/Qualifiers
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/organism="unknown"
BASE COUNT 2 a 6 c 6 g 6 t
ORIGIN
Query Match 58.1%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCTGATTGATGACGAGG 20
Db 18 CCTGACTGAGCACAGG 2

RESULT 13
AX134104/c
LOCUS AX134104 20 bp DNA linear PAT 29-MAY-2001
DEFINITION Sequence 15 from Patent EP1113081.
ACCESSION AX134104
VERSION AX134104.1 GI:14270868
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
source Charrier-Harlin,M.C., Amouyel,P. and Lambert,J.C.
Patent: EP 1113081-A 15 04-JUL-2001;
Institution PASTEUR DE LILLE (FR); INSTITUT NATIONAL DE LA SANTE ET
DE LA RECHERCHE MEDICALE (INSERM) (FR)
Location/Qualifiers
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DEFINITION Sequence 15 from Patent WO0148240.
ACCESSION AX189713
VERSION AX189713.1 GI:15143089
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
source Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
Patent: WO 03025177-A 628 27-MAR-2003;
Molecular Engines Laboratories (FR)
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AUTHORS Charlier-Harlin,M.C., Amouyel,P., Lambert,J.C. and Araria,L.
TITLE Implication of a known gene named cp2/lstf-lbp-1 in Alzheimer's
disease
JOURNAL Patent: WO 0148240-A 15 05-JUL-2001;
INSTITUT PASTEUR DE LILLE (FR) ; INSTITUT NATIONAL DE LA SANTE ET
DE LA RECHERCHE MEDICALE (INSERM) (FR)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Serup,P., Heimberg,H. and Gradwohl,G.
TITLE Method for generating insulin-secreting cells suitable for
transplantation
JOURNAL Patent: WO 02074946-A 60 26-SEP-2002;
NOVO NORDISK A/S (DK)

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Search completed: February 20, 2004, 01:49:33
Job time : 1599.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 21:22:43 ; Search time 2275.5 Seconds
(without alignments)
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Title: US-10-085-108-21_COPY_711_731

Perfect score: 21

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Scoring table: IDENTITY NUC

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C 3	21	100.0	425	36	US-09-864-761-4696 Sequence 4696, Ap
C 4	21	100.0	425	47	US-10-182-993-4749 Sequence 4749, Ap

Sequence 4696, Ap
Sequence 4815, Ap
Sequence 4657, Ap
Sequence 4839, Ap
Sequence 4857, Ap
Sequence 4917, Ap
Sequence 4923, Ap
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Sequence 4922, Ap
Sequence 5855, Ap
Sequence 100997,
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Sequence 1480, Ap
Sequence 24158, A
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Sequence 331, App
Sequence 828, App
Sequence 337, App
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; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: PCT/US01/00663
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
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; LENGTH: 425
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; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4923
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023279.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.3
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
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; FEATURE:
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Best Local Similarity 100.0%; Pred. No. 5.8;
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; GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIORITY FILING DATE: 2001-05-23
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PRIORITY FILING DATE: 2000-02-04
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PRIORITY FILING DATE: 2001-01-29
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SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
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ORGANISM: Homo sapiens
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
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Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: PB 0004 WO 2
CURRENT APPLICATION NUMBER: US/10/182,993
CURRENT FILING DATE: 2002-08-02
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 04 February 2000 (04.02.00)
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 26 May 2000 (26.05.00)
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 03 August 2000 (03.08.00)
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 03 October 2000 (03.10.00)
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 27 September 2000 (27.09.00)
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 21 September 2000 (21.09.00)
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 37811
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 4749
LENGTH: 425
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL023279.1
FEATURE:
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
US-10-182-993-4749
Query Match 100.0%; Score 21; DB 47; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGCCTGATTGATGACCAGG 21
Db 150 AAGCCTGATTGATGACCAGG 130
RESULT 5
US-10-182-995-4696/c
Sequence 4696, Application US/10182995
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: PB 0004 WO 1
CURRENT APPLICATION NUMBER: US/10/182,995
CURRENT FILING DATE: 2002-08-02
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 04 February 2000 (04.02.00)
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 26 May 2000 (26.05.00)
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 03 August 2000 (03.08.00)
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 03 October 2000 (03.10.00)
PRIORITY APPLICATION NUMBER: US 60/236,359

;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 29119
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4696
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023279.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6
US-10-182-995-4696

Query Match 100.0%; Score 21; DB 47; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACCAGG 21
|||
Db 150 AAGCTGATTGATGACCAGG 130

RESULT 6
US-10-182-997-4815/C
; Sequence 4815, Application US/10182997
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 10
; CURRENT APPLICATION NUMBER: US/10/182,997
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 26941
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4815
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023279.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.1
US-10-182-997-4815

Query Match 100.0%; Score 21; DB 47; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACCAGG 21
|||
Db 150 AAGCTGATTGATGACCAGG 130

RESULT 7
US-10-182-998-4657/C
; Sequence 4657, Application US/10182998
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 9
; CURRENT APPLICATION NUMBER: US/10/182,998
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15009
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4657
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023279.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 6.3
US-10-182-998-4657

Query Match 100.0%; Score 21; DB 47; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACCAGG 21
|||
Db 150 AAGCTGATTGATGACCAGG 130

RESULT 8
US-10-203-134-4839/C
; Sequence 4839, Application US/10203134
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 6
; CURRENT APPLICATION NUMBER: US/10/203,134
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; NUMBER OF SEQ ID NOS: 26941
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4815
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023279.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.1
US-10-203-134-4839

Query Match 100.0%; Score 21; DB 47; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACCAGG 21
|||
Db 150 AAGCTGATTGATGACCAGG 130

RESULT 8
US-10-203-134-4839/C
; Sequence 4839, Application US/10203134
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 6
; CURRENT APPLICATION NUMBER: US/10/203,134
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; NUMBER OF SEQ ID NOS: 26941
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4815
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023279.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.1
US-10-203-134-4839

Query Match 100.0%; Score 21; DB 47; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACCAGG 21
|||
Db 150 AAGCTGATTGATGACCAGG 130

;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 38628
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 4839
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
US-10-203-134-4839

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCAGG 21
|||
DB 150 AAGCCTGATTGATGACCAGG 130

RESULT 9
US-10-203-135-4857/c
;; Sequence 4857, Application US/10203135
;; GENERAL INFORMATION:
;; APPLICANT: Molecular Dynamics, Inc.
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: PB 0004 WO 5
;; CURRENT APPLICATION NUMBER: US/10/203,135
;; CURRENT FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 04 February 2000 (04.02.00)
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 26 May 2000 (26.05.00)
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 37012
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 4857
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
US-10-203-135-4857

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCAGG 21
|||

DB 150 AAGCCTGATTGATGACCAGG 130

RESULT 10
US-10-203-136-4917/c
;; Sequence 4917, Application US/10203136
;; GENERAL INFORMATION:
;; APPLICANT: Molecular Dynamics, Inc.
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: PB 0004 WO 3
;; CURRENT APPLICATION NUMBER: US/10/203,136
;; CURRENT FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 04 February 2000 (04.02.00)
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 26 May 2000 (26.05.00)
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 38578
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 4917
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.9
US-10-203-136-4917

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCAGG 21
|||
DB 150 AAGCCTGATTGATGACCAGG 130

RESULT 11
US-10-203-137-4923/c
;; Sequence 4923, Application US/10203137
;; GENERAL INFORMATION:
;; APPLICANT: Molecular Dynamics, Inc.
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: PB 0004 WO 7
;; CURRENT APPLICATION NUMBER: US/10/203,137
;; CURRENT FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 04 February 2000 (04.02.00)
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 26 May 2000 (26.05.00)
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 37012
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 4857
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
US-10-203-135-4857

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCAGG 21
|||

;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 38937
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 4923
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.3
US-10-203-137-4923

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACGAGG 21
Db 150 AAGCTGATTGATGACGAGG 130
|||||

RESULT 12
US-10-203-138-4770/c
;; Sequence 4770, Application US/10203138
;; GENERAL INFORMATION:
;; APPLICANT: Molecular Dynamics, Inc.
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: PB 0004 WO 8
;; CURRENT APPLICATION NUMBER: US/10/203,138
;; CURRENT FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 04 February 2000 (04.02.00)
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 26 May 2000 (26.05.00)
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; NUMBER OF SEQ ID NOS: 15438
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 4770
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.4
US-10-203-138-4770

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACGAGG 21
Db 150 AAGCTGATTGATGACGAGG 130
|||||

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACGAGG 21

Db 150 AAGCTGATTGATGACGAGG 130
|||||

RESULT 13
US-10-203-138A-4770/c
;; Sequence 4770, Application US/10203138A
;; GENERAL INFORMATION:
;; APPLICANT: Molecular Dynamics, Inc.
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: PB 0004 WO 8
;; CURRENT APPLICATION NUMBER: US/10/203,138A
;; CURRENT FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 04 February 2000 (04.02.00)
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 26 May 2000 (26.05.00)
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; NUMBER OF SEQ ID NOS: 15438
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 4770
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.4
US-10-203-138A-4770

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACGAGG 21
Db 150 AAGCTGATTGATGACGAGG 130
|||||

RESULT 14
US-10-203-139-4922/c
;; Sequence 4922, Application US/10203139
;; GENERAL INFORMATION:
;; APPLICANT: Molecular Dynamics, Inc.
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: PB 0004 WO 4
;; CURRENT APPLICATION NUMBER: US/10/203,139
;; CURRENT FILING DATE: 2002-08-02
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 04 February 2000 (04.02.00)
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 26 May 2000 (26.05.00)
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 03 August 2000 (03.08.00)

Db 150 AAGCCTGATTGATGACCCAGGG 130

Search completed: February 20, 2004, 00:32:19
Job time : 2278.5 secs

;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 03 October 2000 (03.10.00)
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 27 September 2000 (27.09.00)
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 21 September 2000 (21.09.00)
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 30 June 2000 (30.06.00)
;; NUMBER OF SEQ ID NOS: 37156
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 4922
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; FEATURE:
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.7
US-10-203-139-4922

Query Match 100.0%; Score 21; DB 48; Length 425;
Best Local Similarity 100.0%; Pred.No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCCTGATTGATGACCCAGGG 21
|||||
Db 150 AAGCCTGATTGATGACCCAGGG 130

RESULT 15
US-60-236-359-5855/c
;; Sequence 5855, Application US/60236359
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: MDMORF-4P
;; CURRENT APPLICATION NUMBER: US/60/236,359
;; CURRENT FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; NUMBER OF SEQ ID NOS: 21709
;; SOFTWARE: Molecular Dynamics Sequence Listing Engine
;; SEQ ID NO 5855
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
;; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 7.1
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.4
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.9
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.7
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.3
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.3
;; OTHER INFORMATION: EST HUMAN HIT: BE276397.1, EVALUATE 8.00e-11
;; OTHER INFORMATION: NT HIT: g1 4885474, EVALUATE 2.00e-78
;; OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUATE 1.00e-42
US-60-236-359-5855

Query Match 100.0%; Score 21; DB 78; Length 425;
Best Local Similarity 100.0%; Pred.No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCCTGATTGATGACCCAGGG 21
|||||

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OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 22:22:13 ; Search time 194 seconds
(without alignments)
398.744 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	100.0	425	9	US-09-864-761-4696
C 2	21	100.0	921	13	US-10-027-632-100997
C 3	21	100.0	921	14	US-10-027-632-100997
C 4	21	100.0	1041	14	US-10-085-108-21
C 5	17.4	82.9	1022	13	US-10-027-632-258115
C 6	17.4	82.9	1022	14	US-10-027-632-258115
C 7	16.8	80.0	504	10	US-09-728-445-868
C 8	16.8	80.0	12591	15	US-10-213-878-6
C 9	16.8	80.0	12591	15	US-10-214-053-6
C 10	16.2	77.1	456	9	US-09-864-761-11491
C 11	16.2	77.1	481	11	US-09-918-995-283
C 12	16.2	77.1	512	13	US-10-027-632-37978
C 13	16.2	77.1	512	13	US-10-027-632-37978
C 14	16.2	77.1	512	14	US-10-027-632-37978
C 15	16.2	77.1	512	14	US-10-027-632-37978

16	16.2	77.1	619	13	US-10-027-632-32980
17	16.2	77.1	619	14	US-10-027-632-32980
18	16.2	77.1	741	13	US-10-027-632-151775
19	16.2	77.1	741	14	US-10-027-632-151775
20	16.2	77.1	1657	13	US-10-027-632-255152
21	16.2	77.1	1657	14	US-10-027-632-255152
22	16.2	77.1	1920	13	US-10-181-157-4
23	16.2	77.1	1920	13	US-09-843-250-12
24	16.2	77.1	6779	11	US-09-843-250-13
25	16.2	77.1	7325	13	US-10-240-965-72
26	15.8	75.2	441	12	US-10-369-493-40614
27	15.8	75.2	470	9	US-09-864-761-5173
28	15.8	75.2	707	13	US-10-027-632-12506
29	15.8	75.2	707	14	US-10-027-632-12506
30	15.8	75.2	809	13	US-10-027-632-153398
31	15.8	75.2	809	14	US-10-027-632-153398
32	15.8	75.2	1343	10	US-09-887-576-481
33	15.8	75.2	1344	10	US-09-887-576-481
34	15.8	75.2	3457	12	US-10-108-260A-1224
35	15.4	73.3	312	10	US-09-738-626-1944
36	15.4	73.3	320	9	US-09-764-887-17
37	15.4	73.3	320	15	US-10-073-961-17
38	15.4	73.3	1185	12	US-10-369-493-43880
39	15.4	73.3	2377	12	US-10-369-493-27069
40	15.4	73.3	2753	9	US-09-764-887-323
41	15.4	73.3	2753	9	US-09-764-887-324
42	15.4	73.3	2753	15	US-10-073-961-323
43	15.4	73.3	2753	15	US-10-073-961-324
44	15.4	73.3	4780	9	US-09-886-241-1
45	15.4	73.3	3309400	10	US-09-738-626-1

ALIGNMENTS

RESULT 1

US-09-864-761-4696/c
; Sequence 4696, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 4696
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL023279.1
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.1
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.4
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.9
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.7
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.3
;; OTHER INFORMATION: EXPRESSED IN HL6100, SIGNAL = 6.3
US-09-864-761-4696

Query Match 100.0%; Score 21; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCCAGG 21
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DB 150 AAGCCTGATTGATGACCCAGG 130

RESULT 2
US-10-027-632-100997/c
; Sequence 100997, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100997
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-100997

Query Match 100.0%; Score 21; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCCAGG 21
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DB 150 AAGCCTGATTGATGACCCAGG 130

RESULT 2
US-10-027-632-100997/c
; Sequence 100997, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100997
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-100997

Query Match 100.0%; Score 21; DB 13; Length 921;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCCAGG 21
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DB 156 AAGCCTGATTGATGACCCAGG 136

RESULT 3
US-10-027-632-100997/c
; Sequence 100997, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100997
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-100997

Query Match 100.0%; Score 21; DB 14; Length 921;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCCAGG 21
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DB 156 AAGCCTGATTGATGACCCAGG 136

RESULT 4
US-10-085-108-21
; Sequence 21, Application US/10085108
; Publication No. US2002017686SAI
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
; FOR
; TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-B
; MAGE-B FAMILIES AND USES THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS

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Best Local Similarity 94.7%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  GCCTGATTGATGACCAGG 21
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Db      969  GCCTGATTGATGACCAGG 951

RESULT 6
US-10-027-632-258115/c
; Sequence 258115, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 258115
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-258115

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, PRIOR FILING DATE: 1999-03-28
, PRIOR APPLICATION NUMBER: US 60/146,002
, PRIOR FILING DATE: 1999-08-09
, NUMBER OF SEQ ID NOS: 325720
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 258115
, LENGTH: 1022
, TYPE: DNA
, ORGANISM: Human
US-10-027-632-258115

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US-10-027-832-238115
Query Match      82.9%; Score 17.4; DB 14; Length 1022;
Best Local Similarity 94.7%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 3 GCCTGATTGATGACCAAGG 21
      |||||..|||||||
Db 969 GCCTGATTGATGACCAAGG 951

RESULT 7
US-09-728-445-868
; Sequence 868, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543A1 Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: JEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 868
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-868

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Query Match 80.0%; Score 16.8; DB 10; Length 504;

Best Local Similarity 90.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCTGATTGATGACCCAGG 21
Db 461 AGCAGGATTGATGACCCAGG 480

RESULT 8
US-10-213-878-6
; Sequence 6, Application US/10213878
; Publication No. US20030073206A1
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; APPLICANT: Nagarajan, Vasantha
; APPLICANT: Thomas, Stuart
; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
; TITLE OF INVENTION: Monocyclic Aromatic Compounds
; FILE REFERENCE: CL1662 US NA
; CURRENT APPLICATION NUMBER: US/10/213,878
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/311,490
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 12591
; TYPE: DNA
; ORGANISM: Sphingomonas sp.
US-10-213-878-6

Query Match 80.0%; Score 16.8; DB 15; Length 12591;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCCAGG 20
Db 7673 AAGCCTGATGATGCCAGG 7692

RESULT 9
US-10-214-059-6
; Sequence 6, Application US/10214059
; Publication No. US2003007768A1
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; APPLICANT: Nagarajan, Vasantha
; APPLICANT: Thomas, Stuart
; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
; TITLE OF INVENTION: Polycyclic Aromatic Compounds
; FILE REFERENCE: CL1663 US NA
; CURRENT APPLICATION NUMBER: US/10/214,059
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/311,486
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 12591
; TYPE: DNA
; ORGANISM: Sphingomonas sp.
US-10-214-059-6

Query Match 80.0%; Score 16.8; DB 15; Length 12591;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCCAGG 20
Db 7673 AAGCCTGATGATGCCAGG 7692

RESULT 10

US-09-864-761-11491
; Sequence 11491, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11491
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005739.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
US-09-864-761-11491

Query Match 77.1%; Score 16.2; DB 9; Length 456;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACCCAGG 21
Db 15 ATGCTGATTGATTCCAGG 35

RESULT 11

US-09-918-995-283
; Sequence 283, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 283
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(481)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-283

Query Match 77.1%; Score 16.2; DB 11; Length 481;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACGAGG 21

DB 204 AAGCATGATTGAAGACGAGG 224

RESULT 12

US-10-027-632-37978/c
; Sequence 37978, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37978
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-37978

Query Match 77.1%; Score 16.2; DB 13; Length 512;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACGAGG 21

DB 126 AAGCATGTTGGATGACGAGG 106

RESULT 13

US-10-027-632-76583/c
; Sequence 76583, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76583
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-76583

Query Match 77.1%; Score 16.2; DB 13; Length 512;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACGAGG 21

DB 126 AAGCATGTTGGATGACGAGG 106

RESULT 14

US-10-027-632-37978/c
; Sequence 37978, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37978

; LENGTH: 512
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-37978

Query Match 77.1%; Score 16.2; DB 14; Length 512;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACACGGG 21
|||||
Db 126 AAGCATGGTGGATGACACGGG 106

RESULT 15

US-10-027-632-76583/c
; Sequence 76583, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76583
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-76583

Query Match 77.1%; Score 16.2; DB 14; Length 512;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTGATTGATGACACGGG 21
|||||
Db 126 AAGCATGGTGGATGACACGGG 106

Search completed: February 20, 2004, 00:50:07
Job time : 197 secs

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OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 21:14:23 ; Search time 46 Seconds
(without alignments)
201.501 Million cell updates/sec

Title: US-10-085-108-21_COPY_711_731

Perfect score: 21

Sequence: 1 AAGCCTGATTGATGACCAGG 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.2	72.4	771	4	US-09-252-991A-13016
C 2	15.2	72.4	2325	1	US-08-019-870-2
C 3	15.2	72.4	2325	1	US-08-019-870-4
C 4	15.2	72.4	2325	1	US-08-019-870-7
C 5	15.2	72.4	2325	1	US-08-019-870-10
C 6	15.2	72.4	2325	1	US-08-314-309A-20
C 7	15.2	72.4	2325	1	US-08-633-760-43
C 8	15.2	72.4	2325	1	US-08-633-760-45
C 9	15.2	72.4	2325	1	US-08-633-760-47
C 10	15.2	72.4	2325	1	US-08-633-760-49
C 11	15.2	72.4	2325	1	US-08-633-760-51
C 12	15.2	72.4	2373	1	US-08-019-870-9
C 13	15.2	72.4	2665	3	US-09-040-005-1
C 14	15.2	72.4	2847	1	US-07-747-501A-2
C 15	15.2	72.4	2847	1	US-07-935-312-2
C 16	15.2	72.4	5860	4	US-09-221-017B-820
C 17	15	71.4	541	4	US-09-404-879A-108
C 18	15	71.4	541	4	US-09-338-933-108
C 19	15	71.4	541	4	US-09-215-681-108
C 20	15	71.4	7210	4	US-09-634-238-15
C 21	14.8	70.5	423	1	US-08-470-179-129
C 22	14.8	70.5	423	4	US-09-252-991A-3094
C 23	14.8	70.5	443	1	US-08-592-406-13
C 24	14.8	70.5	591	4	US-09-280-116-138
C 25	14.8	70.5	600	4	US-09-107-532A-2277
C 26	14.8	70.5	654	4	US-09-252-991A-2992
C 27	14.8	70.5	725	3	US-09-197-801-12

C 28	14.8	70.5	725	3	US-09-551-028-12	Sequence 12, Appl
C 29	14.8	70.5	1126	2	US-08-479-733A-27	Sequence 27, Appl
C 30	14.8	70.5	1126	3	US-08-487-427-27	Sequence 27, Appl
C 31	14.8	70.5	1126	3	US-08-479-727A-27	Sequence 27, Appl
C 32	14.8	70.5	1126	3	US-08-482-369A-27	Sequence 27, Appl
C 33	14.8	70.5	1126	5	PCT-US95-07439-27	Sequence 27, Appl
C 34	14.8	70.5	1404	3	US-09-202-101-15	Sequence 15, Appl
C 35	14.8	70.5	1467	4	US-09-367-777-43	Sequence 43, Appl
C 36	14.8	70.5	1467	4	US-09-367-791A-26	Sequence 26, Appl
C 37	14.8	70.5	1500	1	US-08-487-037-4	Sequence 4, Appl
C 38	14.8	70.5	1536	4	US-09-252-991A-3182	Sequence 3182, Ap
C 39	14.8	70.5	1932	4	US-09-640-198D-1	Sequence 1, Appl
C 40	14.8	70.5	2070	4	US-09-252-991A-2687	Sequence 2687, Ap
C 41	14.8	70.5	4080	4	US-09-016-434-1346	Sequence 1346, Ap
C 42	14.8	70.5	5836	4	US-09-453-702B-253	Sequence 253, App
C 43	14.8	70.5	8554	4	US-09-221-017B-523	Sequence 523, App
C 44	14.8	70.5	12848	4	US-09-453-702B-252	Sequence 252, App
C 45	14.8	70.5	13158	2	US-08-687-080-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-09-252-991A-13016/c
; Sequence 13016, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13016
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13016

Query Match 72.4%; Score 15.2; DB 4; Length 771;
Best Local Similarity 85.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3;
QY 1 AAGCCTGATTGATGACCAGG 20
|||||
Db 208 AAGCCTGTTCTGACCAGG 189

RESULT 2
US-08-019-870-2/c
; Sequence 2, Application US/08019870
; Patent No. 5336613
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: YOSHIMASA, SAITO
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: ISHII, YOSHINORI
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/019,870
; FILING DATE: 19930219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5336613man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-791-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2322
; NAME/KEY: mat_peptide
; LOCATION: 4..2322
; US-08-019-870-2
;
; Query Match 72.4%; Score 15.2; DB 1; Length 2325;
; Best Local Similarity 85.0%; Pred. No. 1.2e+02;
; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 AAGCGTGATTGATGACGAGG 20
; Db 1546 AAGCGGATTGGCGACGAGG 1527
;
; RESULT 3
; US-08-019-870-4/c
; Sequence 4, Application US/08019870
; Patent No. 5336613
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: YOSHIMASA, SAITO
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: ISHII, YOSHINORI
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/019,870
; FILING DATE: 19930219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5336613man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-791-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; REFERENCE/DOCKET NUMBER: 18-791-0
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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2322
; NAME/KEY: mat_peptide
; LOCATION: 4..2322
; US-08-019-870-4
;
; Query Match 72.4%; Score 15.2; DB 1; Length 2325;
; Best Local Similarity 85.0%; Pred. No. 1.2e+02;
; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 AAGCGTGATTGATGACGAGG 20
; Db 1546 AAGCGGATTGGCGACGAGG 1527
;
; RESULT 4
; US-08-019-870-7/c
; Sequence 7, Application US/08019870
; Patent No. 5336613
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: YOSHIMASA, SAITO
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: ISHII, YOSHINORI
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/019,870
; FILING DATE: 19930219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5336613man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-791-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
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LOCATION: 1..2322
FEATURE:
NAME/KEY: mat peptide
LOCATION: 4..2322
US-08-019-870-7

Query Match 72.4%; Score 15.2; DB 1; Length 2325;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGCCTGATTGATGCCAGG 20
Db 1546 AAGCCGGATTGGCAGCAGG 1527

RESULT 5

US-08-019-870-10/c
Sequence 10, Application US/08019870
Patent No. 5336613
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: YOSHIMASA, SAITO
APPLICANT: SASAKI, HITOSHI
APPLICANT: ISHII, YOSHINORI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
City: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/019,870
FILING DATE: 19930219
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5336613man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-791-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 1..2322
FEATURE:
NAME/KEY: mat peptide
LOCATION: 4..2322

US-08-019-870-10

Query Match 72.4%; Score 15.2; DB 1; Length 2325;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGCCTGATTGATGCCAGG 20
Db 1546 AAGCCGGATTGGCAGCAGG 1527

RESULT 6

US-08-314-309A-20/c
Sequence 20, Application US/08314309A
Patent No. 5677141

GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: FUKAGAWA, MASAO
APPLICANT: IWAMI, MORITA
APPLICANT: ARAMORI, ICHIRO
APPLICANT: KOJO, HITOSHI
TITLE OF INVENTION: PROCESS FOR PRODUCING 7-AMINOCEPHEM
TITLE OF INVENTION: COMPOUND OR SALTS THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
City: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,309A
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631,906
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5677141man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-863-0 CONT

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 1..2322
US-08-314-309A-20

Query Match 72.4%; Score 15.2; DB 1; Length 2325;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGCCTGATTGATGCCAGG 20
Db 1546 AAGCCGGATTGGCAGCAGG 1527

RESULT 7

US-08-633-760-43/c
Sequence 43, Application US/08633760
Patent No. 5804429

GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: ISHII, YOSHINORI

APPLICANT: NOGUCHI, YUJI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2325
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 4..2322
US-08-633-760-45

Query Match 72.4%; Score 15.2; DB 1; Length 2325;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AGCCCTGATTGATGACCAGG 20
||||| ||||| ||||| ||||| |||||
Db 1546 AAGCCGGATTGGCAGCAGG 1527

RESULT 8
US-08-633-760-45/c
Sequence 45, Application US/08633760
Patent No. 5804429
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: ISHII, YOSHINORI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2325
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 4..2322
US-08-633-760-45
Query Match 72.4%; Score 15.2; DB 1; Length 2325;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AGCCCTGATTGATGACCAGG 20
||||| ||||| ||||| ||||| |||||
Db 1546 AAGCCGGATTGGCAGCAGG 1527
RESULT 9
US-08-633-760-47/c
Sequence 47, Application US/08633760
Patent No. 5804429
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: ISHII, YOSHINORI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2325
FEATURE:
NAME/KEY: mat peptide
LOCATION: 4..2322
US-08-633-760-47

Query Match 72.4%; Score 15.2; DB 1; Length 2325;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCCTGATTGATGACCAGG 20
||||| ||||| ||||| |||||
DB 1546 AAGCCGATTGGCAGCAGG 1527

RESULT 10

US-08-633-760-49/c
Sequence 49, Application US/08633760
Patent No. 5804429
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: ISHII, YOSHINORI
APPLICANT: NOGUCHI, YUJI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 1..2325
FEATURE:
NAME/KEY: mat peptide
LOCATION: 4..2322
US-08-633-760-49

Query Match 72.4%; Score 15.2; DB 1; Length 2325;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCCTGATTGATGACCAGG 20
||||| ||||| ||||| |||||
DB 1546 AAGCCGATTGGCAGCAGG 1527

RESULT 11

US-08-633-760-51/c
Sequence 51, Application US/08633760
Patent No. 5804429
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: ISHII, YOSHINORI
APPLICANT: NOGUCHI, YUJI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2325
FEATURE:
NAME/KEY: mat peptide
LOCATION: 4..2322
US-08-633-760-51

Query Match 72.4%; Score 15.2; DB 1; Length 2325;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCCTGATTGATGACCAGG 20

Db 1546 AAGCGGATTGGCAGCAGG 1527
||||| ||||| |||||

RESULT 12

US-08-019-870-9/c
; Sequence 9, Application US/08019870
; Patent No. 5336613
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: YOSHINAKA, SAITO
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: ISHII, YOSHINOBU
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/019,870
; FILING DATE: 19930219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5336613man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-791-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-019-870-9

Query Match 72.4%; Score 15.2; DB 1; Length 2373;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCGGATTGGCAGCAGG 20
||||| ||||| |||||
Db 1594 AAGCGGATTGGCAGCAGG 1575

RESULT 13

US-09-040-005-1
; Sequence 1, Application US/09040005
; Patent No. 6057128
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA

; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,005
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15320
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8224
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-040-005-1

Query Match 72.4%; Score 15.2; DB 3; Length 2665;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCTGATTGATGACGAGG 21
||||| ||||| |||||
Db 50 AGCCTGATTGATGACGAGG 69

RESULT 14

US-07-747-901A-2/c
; Sequence 2, Application US/07747901A
; Patent No. 5192678
; GENERAL INFORMATION:
; APPLICANT: Iwami, Morita
; APPLICANT: Aramori, Ichiro
; APPLICANT: Fukagawa, Masao
; APPLICANT: Isogai, Takao
; APPLICANT: Kojo, Hitoshi
; TITLE OF INVENTION: CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/747,901A
; FILING DATE: 19910820
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5192678man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-709-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-4500
; TELEFAX: (703) 486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

Db 2028 AAGCCGGATTGGCGACCAGG 2009
Search completed: February 19, 2004, 23:16:14
Job time : 47 secs

LENGTH: 2847 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 483..2804
US-07-747-901A-2

Query Match 72.4%; Score 15.2; DB 1; Length 2847;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACCAGG 20
Db 2028 AAGCCGGATTGGCGACCAGG 2009

RESULT 15
US-07-935-312-2/c
Sequence 2, Application US/07935312
Patent No. 5320948
GENERAL INFORMATION:
APPLICANT: Iwami, Morita
APPLICANT: Aramori, Ichiro
APPLICANT: Fukagawa, Masao
APPLICANT: Isogai, Takao
APPLICANT: Kojo, Hitoshi
TITLE OF INVENTION: CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/935,312
FILING DATE: 19920826
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5320948man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-769-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2847 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 483..2804
US-07-935-312-2

Query Match 72.4%; Score 15.2; DB 1; Length 2847;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGCTGATTGATGACCAGG 20
||||| ||||| |||||

